

## FIGURE 1

GGCATCTGCCCCGAGGAGACCACGCTCCTGGAGCTCTGCTGTCTTCTCAGGGAGACTCTGAGG  
CTCTGTTGAGAATCATGCTTTGGAGGCAGCTCATCTATTGGCAACTGCTGGCTTTGTTTTTC  
CTCCCTTTTTTGCTGTGTCAAGATGAATACATGGAGTCTCCACAAACCGGAGGACTACCCCC  
AGACTGCAGTAAGTGTGTCATGGAGACTACAGCTTTCGAGGCTACCAAGGCCCCCCTGGGC  
CACCGGGCCCTCCTGGCATTCCAGGAAACCATGGAAACAATGGCAACAATGGAGCCACTGGT  
CATGAAGGAGCCAAAGGTGAGAAGGGCGACAAAGGTGACCTGGGGCCTCGAGGGGAGCGGGG  
GCAGCATGGCCCCAAAGGAGAGAAGGGCTACCCGGGGATTCCACCAGAACTTCAGATTGCAT  
TCATGGCTTCTCTGGCAACCCACTTCAGCAATCAGAACAGTGGGATTATCTTCAGCAGTGTT  
GAGACCAACATTGGAAACTTCTTTGATGTCATGACTGGTAGATTTGGGGCCCCAGTATCAGG  
TGTGTATTTCTTCACCTTCAGCATGATGAAGCATGAGGATGTTGAGGAAGTGTATGTGTACC  
TTATGCACAATGGCAACACAGTCTTCAGCATGTACAGCTATGAAATGAAGGGCAAATCAGAT  
ACATCCAGCAATCATGCTGTGCTGAAGCTAGCCAAAGGGGATGAGGTTTGGCTGCGAATGGG  
CAATGGCGCTCTCCATGGGGACCACCAACGCTTCTCCACCTTTGCAGGATTCCTGCTCTTTG  
AACTAAGTAAATATATGACTAGAATAGCTCCACTTTGGGGAAGACTTGTAGCTGAGCTGAT  
TTGTTACGATCTGAGGAACATTAAAGTTGAGGGTTTTACATTGCTGTATTCAAAAAATTATT  
GGTTGCAATGTTGTTACGCTACAGGTACACCAATAATGTTGGACAATTCAGGGGCTCAGAA  
GAATCAACCACAAAATAGTCTTCTCAGATGACCTTGACTAATACTCAGCATCTTTATCAC  
TCTTTCCTTGGCACCTAAAAGATAATTCTCCTCTGACGCAGGTTGGAAATATTTTTTTCTAT  
CACAGAAGTCATTTGCAAAGAATTTTGACTACTCTGCTTTTAATTTAATACCAGTTTTTCAGG  
AACCCTGAAGTTTTAAGTTCATTATTCTTTATAACATTTGAGAGAATCGGATGTAGTGATA  
TGACAGGGCTGGGGCAAGAACAGGGGCACTAGCTGCCTTATTAGCTAATTTAGTGCCCTCCG  
TGTTTCAGCTTAGCCTTTGACCCTTTCCTTTTGATCCACAAAATACATTAAAACTCTGAATTC  
ACATACAATGCTATTTTAAAGTCAATAGATTTTAGCTATAAAGTGCTTGACCAGTAATGTGG  
TTGTAATTTTGTGTATGTTCCCCCACATCGCCCCCAACTTCGGATGTGGGGTCAGGAGGTTG  
AGGTTCACTATTAACAAATGTCATAAATATCTCATAGAGGTACAGTGCCAATAGATATTCAA  
ATGTTGCATGTTGACCAGAGGGATTTTATATCTGAAGAACATACACTATTAATAAATACCTT  
AGAGAAAGATTTTGACCTGGCTTTAGATAAAACTGTGGCAAGAAAAATGTAATGAGCAATAT  
ATGGAAATAAACACACCTTTGTTAAAGATAAAAAAAA

## **FIGURE 2**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44686

><subunit 1 of 1, 246 aa, 1 stop

><MW: 26994, pI: 6.43, NX(S/T): 0

MLWRQLIYWQLLALFFLPFCLCQDEYMESPQTGGLPPDCSKCCHGDYSFRGYQGPPGPPGPP  
GIPGNHGNNGNNGATGHEGAKGEKGDKGDLGPRGERGQHGPKEKGYPGIPPPELQIAFMASL  
ATHFSNQNSGIIFFSSVETNIGNFFDVMGTGRFGAPVSGVYFFTFSMMKHEDVEEVYVYLMHNG  
NTVFMSYEMKGKSDTSSNHAVLKLAKGDEVWLRMGNGALHGDHQRSTFAGFLLFETK

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-22

#### **Motif name: Clq domain signature.**

amino acids 137-167

#### **Clq domain proteins.**

amino acids 135-169, 202-221, 235-244, 57-91, 60-94, 54-88, 81-114, 78-111, 63-96, 51-84, 45-78, 48-81, 33-66, 66-99 and 42-75

### FIGURE 3

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTTGCAAGGCGACAGCTGTGCCAGCCGGG  
CTCTGGCAGGCTCCTGGCAGCATGGCAGTGAAGCTTGGGACCCTCCTGCTGGCCCTTGCCCT  
GGGCCTGGCCCAGCCAGCCTCTGCCCCGCCGGAAGCTGCTGGTGTCTCTGCTGGATGGTTTTT  
GCTCAGACTACATCAGTGATGAGGCGCTGGAGTCATTGCCTGGTTTTCAAAGAGATTGTGAGC  
AGGGGAGTAAAAGTGGATTACTTGACTCCAGACTTCCCTAGTCTCTCGTATCCCAATTATTA  
TACCCTAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACTACATGTGGGACC  
CCACCACCAACAAGTCCTTTGACATTGGCGTCAACAAAGACAGCCTAATGCCTCTCTGGTGG  
AATGGATCAGAACCTCTGTGGGTCACTCTGACCAAGGCCAAAAGGAAGGTCTACATGTACTA  
CTGGCCAGGCTGTGAGGTTGAGATTCTGGGTGTCAGACCCACCTACTGCCTAGAATATAAAA  
ATGTCCCAACGGATATCAATTTTGCCAATGCAGTCAGCGATGCTCTTGACTCCTTCAAGAGT  
GGCCGGGCGGACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCACTACGG  
GCCTGCATCTCCGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCCTGAAGTACATGA  
CCAAGTGGATCCAGGAGCGGGGCTGCAGGACCGCCTGAACGTCATTATTTTCTCGGATCAC  
GGAATGACCGACATTTTCTGGATGGACAAAGTGATTGAGCTGAATAAGTACATCAGCCTGAA  
TGACCTGCAGCAAGTGAAGGACCGCGGGCCTGTTGTGAGCCTTTGGCCGGCCCCCTGGGAAAC  
ACTCTGAGATATATAACAACTGAGCACAGTGGAACACATGACTGTCTACGAGAAAGAAGCC  
ATCCCAAGCAGGTTCTATTACAAGAAAGGAAAGTTTGTCTCTCCTTTGACTTTAGTGGCTGA  
TGAAGGCTGGTTCATAACTGAGAATCGAGAGATGCTTCCGTTTTGGATGAACAGCACCGGCA  
GGCGGGAAGGTTGGCAGCGTGGATGGCACGGCTACGACAACGAGCTCATGGACATGCGGGGC  
ATCTTCCTGGCCTTCGGACCTGATTTCAAATCCAACCTTCAGAGCTGCTCCTATCAGGTCGGT  
GGACGTCTACAATGTCATGTGCAATGTGGTGGGCATCACCCCGCTGCCCCAACAACGGATCCT  
GGTCCAGGGTGATGTGCATGCTGAAGGGCCGCGCCGGCACTGCCCCGCCTGTCTGGCCCAGC  
CACTGTGCCCTGGCACTGATTCTTCTCTTCCTGCTTGCATAACTGATCATATTGCTTGTCTC  
AGAAAAAACACCATCAGCAAAGTGGGCCTCCAAAGCCAGATGATTTTCATTTTATGTGTGA  
ATAATAGCTTCATTAACACAATCAAGACCATGCACATTGTAAATACATTATTCTTGGATAAT  
TCTATACATAAAAGTTCCTACTTGTTAAA

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## **FIGURE 4**

MAVKLGTLALLALGLAQPASARRKLLVFLLDGFRSDYISDEALES LPGFKEIVSRGVKVDY  
LTPDFPSLSYPNYYTLMTGRHCEVHQMIGNYMWDPTTNKSFDIGVNKDSL MPLWWNGSEPLW  
VTLTKAKRKVYMYYPGCEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSFKSGRADLAA  
IYHERIDVEGHHYGPASPQRKDALKAVDTVLKYMTKWIQERGLQDRLNVII FSDHGMTDIFW  
MDKVIELNKYISLNDLQQVKDRGPVVSLWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFY  
KKGK FVSPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGWHGYDNELMDMRGIFLAFGP  
DFKSNFRAAPIRSVDVYNVMCNVVGITPLPNNGSWSRVMCMLKGRAGTAPPVWPSHCALALI  
LLFLLA

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-22

#### **N-glycosylation sites.**

amino acids 100-104, 118-122, 341-345, 404-408

#### **N-myristoylation sites.**

amino acids 148-154, 365-371

#### **Amidation site.**

amino acids 343-347

[illegible][illegible]

## **FIGURE 6**

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHELLARGAKWGQAL  
PVALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRYRVDTDEDYPQKL  
AFAECLCRGCIDARTGRETAALNSVRLQLSLLVLRRRRPCSRDGSGGLPTPGAFAFHTEFIHVP  
VGCTCVLPRSV

**Important features:**

**Signal peptide:**

amino acids 1-18

**Tyrosine kinase phosphorylation site.**

amino acids 112-121

**N-myristoylation sites.**

amino acids 32-38, 55-61, 133-139

**Leucine zipper pattern.**

amino acids 3-25

**Homologous region to IL-17.**

amino acids 99-195

## **FIGURE 7**

CGGCCAGGGCGCCGACAGCCCGACCTCACCAGGAGAAC**ATG**CAGCTCGGGCACTGGGCTCCTG  
CTGGCCGCCGTCCTGAGCCTGCAGCTGGCTGCAGCCGAAGCCATATGGTGTCAACAGTGCAC  
GGGCTTCGGAGGGTGCTCCCATGGATCCAGATGCCTGAGGGACTCCACCCACTGTGTCACCA  
CTGCCACCCGGGTCCTCAGCAACACCGAGGATTTGCCTCTGGTCAACCAAGATGTGCCACATA  
GGCTGCCCCGATATCCCCAGCCTGGGCCTGGGCCCCCTACGTATCCATCGCTTGCTGCCAGAC  
CAGCCTCTGCAACCATGAC**TGA**CGGCTGCCCTCCTCCAGGCCCCCGGACGCTCAGCCCCAC  
AGCCCCACAGCCTGGCGCCAGGGCTCACGGCCGCCCCCTCCCTCGAGACTGGCCAGCCCACC  
TCTCCCGGCCTCTGCAGCCACCGTCCAGCACCGCTTGTCCTAGGGAAGTCCTGCGTGGAGTC  
TTGCCTCAATCTGCTGCCGTCCAAGCCTGGGGCCCATCGTGCCTGCCGCCCCCTTCAGGTCCC  
GACCTCCCCACAATAAAATGTGATTGGATCGTGTGGTACAAAAAAAAAAAAAAAAAAAAAAAAA  
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><subunit 1 of 1, 97 aa, 1 stop

MQLGTGLLLAAVLSLQLAAAEAIWCHQCTGFGGCSHGSRCLRDSTHCVTATRVLSNTEDLP

Important features of the protein:

amino acids 1-20

amino acids 6-11 and 33-38

## amino acids 24-34 and 78-88



## FIGURE 9

CCAGGACCAGGGCGCACCCGGCTCAGCCTCTCACTTGTGTCAGAGGCCGGGGAAGAGAAGCAAAG  
CGCAACGGTGTGGTCCAAGCCGGGGCTTCTGCTTCGCCTCTAGGACATACACGGGACCCCCCT  
AACTTCAGTCCCCCAAACGCGCACCCCTCGAAGTCTTGAAGTCCAGCCCCGCACATCCACGCG  
CGGCACAGGCGCGGCAGGCGGCAGGTCCCGGCCGAAGGCGATGCGCGCAGGGGGTCTGGGCAG  
CTGGGCTCGGGCGGCGGGAGTAGGGCCCCGGCAGGGAGGCAGGGAGGCTGCATATTCAGAGTC  
GCGGGCTGCGCCCTGGGCAGAGGCCGCCCTCGCTCCACGCAACACCTGCTGCTGCCACCGCG  
CCGCGATGAGCCGCGTGGTCTCGCTGCTGCTGGGCGCCGCGCTGCTCTGCGGCCACGGAGCC  
TTCTGCCGCCGCGTGGTCAGCGGCCAAAAGGTGTGTTTTGCTGACTTCAAGCATCCCTGCTA  
CAAAATGGCCTACTTCCATGAACTGTCCAGCCGAGTGAGCTTTCAGGAGGCACGCCTGGCTT  
GTGAGAGTGAGGGAGGAGTCCTCCTCAGCCTTGAGAATGAAGCAGAACAGAAGTTAATAGAG  
AGCATGTTGCAAAACCTGACAAAACCCGGGACAGGGATTTCTGATGGTGATTTCTGGATAGG  
GCTTTGGAGGAATGGAGATGGGCAAACATCTGGTGCCTGCCCAGATCTCTACCAGTGGTCTG  
ATGGAAGCAATTCCCAGTACCGAAACTGGTACACAGATGAACCTTCCTGCGGAAGTGAAAAG  
TGTGTTGTGATGTATCACCAACCAACTGCCAATCCTGGCCTTGGGGGTCCCTACCTTTACCA  
GTGGAATGATGACAGGTGTAACATGAAGCACAATTATATTTGCAAGTATGAACCAGAGATTA  
ATCCAACAGCCCCCTGTAGAAAAGCCTTATCTTACAAATCAACCAGGAGACACCCATCAGAAT  
GTGGTTGTTACTGAAGCAGGTATAATTCCCAATCTAATTTATGTTGTTATACCAACAATACC  
CCTGCTCTTACTGATACTGGTTGCTTTTGGAACTGTTGTTTCCAGATGCTGCATAAAAGTA  
AAGGAAGAACAAAACTAGTCCAAACCAGTCTACACTGTGGATTTCAAAGAGTACCAGAAAA  
GAAAGTGGCATGGAAGTATAATAACTCATTGACTTGGTTCCAGAATTTTGTAAATTCTGGATC  
TGTATAAGGAATGGCATCAGAACAATAGCTTGGAAATGGCTTGAAATCACAAAGGATCTGCAA  
GATGAACTGTAAGCTCCCCCTTGAGGCAAATATTAAAGTAATTTTTATATGTCTATTATTTT  
ATTTAAAGAATATGCTGTGCTAATAATGGAGTGAGACATGCTTATTTTGCTAAAGGATGCAC  
CCAACTTCAAACCTTCAAGCAAATGAAATGGACAATGCAGATAAAGTTGTTATCAACACGTC  
GGGAGTATGTGTGTTAGAAGCAATTCCTTTTATTTCTTTCACCTTTCATAAGTTGTTATCTA  
GTCAATGTAATGTATATTGTATTGAAATTTACAGTGTGCAAAGTATTTTACCTTTGCATAA  
GTGTTTGATAAAAAATGAACTGTTCTAATATTTATTTTATGGCATCTCATTTTTTCAATACAT  
GCTCTTTTGATTAAAGAACTTATTACTGTTGTCAACTGAATTCACACACACACAAATATAG  
TACCATAGAAAAAGTTTGTCTTCTCGAAATAATTCATCTTTCAGCTTCTCTGCTTTTGGTCA  
ATGTCTAGGAAATCTCTTCAGAAATAAGAAGCTATTTTATTAAGTGTGATATAAACCTCCTC  
AAACATTTTACTTAGAGGCAAGGATTGTCTAATTTCAATTGTGCAAGACATGTGCCTTATAA  
TTATTTTTAGCTTAAAATTAAACAGATTTTGTAAATAATGTAACCTTTGTTAATAGGTGCATAA  
ACACTAATGCAGTCAATTTGAACAAAAGAAGTGACATACACAATATAAATCATATGTCTTCA  
CACGTTGCCTATATAATGAGAAGCAGCTCTCTGAGGGTTCTGAAATCAATGTGGTCCCTCTC  
TTGCCCACTAAACAAAGATGGTTGTTTCGGGGTTTGGGATTGACACTGGAGGCAGATAGTTGC  
AAAGTTAGTCTAAGGTTTCCCTAGCTGTATTTAGCCTCTGACTATATTAGTATACAAAGAGG  
TCATGTGGTTGAGACCAGGTGAATAGTCACTATCAGTGTGGAGACAAGCACAGCACACAGAC  
ATTTTAGGAAGGAAAGGAACTACGAAATCGTGTGAAAATGGGTTGGAACCCATCAGTGATCG  
CATATTCATTGATGAGGGTTTGCTTGAGATAGAAAATGGTGGCTCCTTTCTGTCTTATCTCC  
TAGTTTCTTCAATGCTTACGCCTTGTTCTTCTCAAGAGAAAGTTGTAACCTCTCTGGTCTTCA  
TATGTCCCTGTGCTCCTTTTAACCAAATAAAGAGTTCTTGTTTCTGGGGGAAAAAAAAAAAAA  
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 10**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79230

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30431, pI: 6.79, NX(S/T): 3

MSRVVSLLLGAALLCGHGAFCRRVVGQKVCFADEFKHPCYKMAYFHELSSRVSFQEARLACE  
SEGGVLLSLENEAEQKLIESMLQNLTKPGTGISDGDFWIGLWRNGDGQTSGACPDLYQWSDG  
SNSQYRNWYTDEPSCGSEKCVVMYHQPTANPGLGGPYLYQWNDDRCNMKHNYICKYEPEINP  
TAPVEKPYLTNQP GDTHQNVVVTEAGIIPNLIYVVIPTIPLLLLILVAFGTCCFQMLHKSKG  
RTKTSPNQSTLWISKSTRKESGMEV

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-21

#### **Transmembrane domain:**

amino acids 214-235

#### **N-glycosylation sites.**

amino acids 86-89 and 255-258

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 266-269

#### **N-myristoylation sites.**

amino acids 27-32, 66-71, 91-96, 93-98, 102-107, 109-114, 140-145  
and 212-217

## FIGURE 11

GGAGAATGGAGAGAGCAGTGAGAGTGGAGTCCGGGGTCTGGTCCGGGGTGGTCTGTCTGCTCCTGGCATGCCCTG  
CCACAGCCACTGGGCCCCGAAGTTGCTCAGCCTGAAGTAGACACCACCCTGGGTCTGTGCGAGGCCGGCAGGTGG  
GCGTGAAGGGCACAGACCGCCTTGTGAATGTCTTTCTGGGCATTCCATTTGCCAGCCGCCACTGGGCCCCTGACC  
GGTTCTCAGCCCCACACCCAGCACAGCCCTGGGAGGGTGTGCGGGATGCCAGCACTGCGCCCCCAATGTGCCTAC  
AAGACGTGGAGAGCATGAACAGCAGCAGATTTGTCCTCAACGGAAAACAGCAGATCTTCTCCGTTTCAGAGGACT  
GCCTGGTCTCAACGTCTATAGCCCAGCTGAGGTCCCCGCAGGGTCCGGTAGGCCGGTCATGGTATGGGTCCATG  
GAGGCGCTCTGATAACTGGCGCTGCCACCTCCTACGATGGATCAGCTCTGGCTGCCTATGGGGATGTGGTCGTGG  
TTACAGTCCAGTACCGCCTTGGGGTCTTGGCTTCTTCAGCACTGGAGATGAGCATGCACCTGGCAACCAGGGCT  
TCCTAGATGTGGTAGCTGCTTTGCGCTGGGTGCAAGAAAACATCGCCCCCTTCGGGGGTGACCTCAACTGTGTCA  
CTGTCTTTGGTGGATCTGCCGGTGGGAGCATCATCTCTGGCCTGGTCTGTCCCCAGTGGCTGCAGGGCTGTTCC  
ACAGAGCCATCACACAGAGTGGGGTCTACACACCCAGGGATCATCGACTCTCACCTTGGCCCCCTAGCTCAGA  
AAATCGCAAACACCTTGGCCTGCAGCTCCAGCTCCCCGGCTGAGATGGTGCAGTGCCTTCAGCAGAAAGAAGGAG  
AAGAGCTGGTCTTAGCAAGAAGCTGAAAAATACTATCTATCCTCTCACCGTTGATGGCACTGTCTTCCCCAAAA  
GCCCCAAGGAACCTCTGAAGGAGAAGCCCTTCCACTCTGTGCCCTTCTCATGGGTGTCAACAACCATGAGTTCA  
GCTGGCTCATCCCCAGGGGCTGGGGTCTCCTGGATAACAATGGAGCAGATGAGCCGGGAGGACATGCTGGCCATCT  
CAACACCCGTCTTGACCACTCTGGATGTGCCCCCTGAGATGATGCCACCGTCATAGATGAATACCTAGGAAGCA  
ACTCGGACGCACAAGCCAAATGCCAGGCGTTCCAGGAATTCATGGGTGACGTATTCATCAATGTTCCACCGTCA  
GTTTTTCAAGATACCTTCGAGATTCTGGAAGCCCTGTCTTTTTCTATGAGTTCCAGCATCGACCCAGTTCTTTTG  
CGAAGATCAAACCTGCCTGGGTGAAGGCTGATCATGGGGCCGAGGGTGCTTTTGTGTTCCGAGGTCCCTTCCTCA  
TGGACGAGAGCTCCCGCCTGGCCTTTCCAGAGGCCACAGAGGAGGAGAAGCAGCTAAGCCTCACCATGATGGCCC  
AGTGGACCCACTTTGCCCGGACAGGGGACCCCAATAGCAAGGCTCTGCCTCCTTGGCCCCAATTCAACCAGGCGG  
AACAATATCTGGAGATCAACCCAGTGCCACGGGCGGACAGAAAGTTCAGGGAGGCCTGGATGCAGTTCTGGTCAG  
AGACGCTCCCCAGCAAGATAACAAGTGGCACCAGAAGCAGAAGAAGCAGGAAGGCCAGGAGGACCTCTGAGGGCC  
AGGCCTGAACCTTCTTGGCTGGGGCAAACCACTCTTCAAGTGGTGGCAGAGTCCCAGCACGGCAGCCCGCCTCTC  
CCCCTGCTGAGACTTTAATCTCCACCAGCCCTTAAAGTGTGCGCCGCTCTGTGACTGGAGTTATGCTCTTTTGAA  
ATGTCACAAGGCCGCTCCACCTCTGGGGCATTGTACAAGTTCTTCCCTCTCCCTGAAGTGCCTTTCTGCTTT  
CTTCGTGGTAGGTTCTAGCACATTCCTCTAGCTTCTTGGAGGACTCACTCCCCAGGAAGCCTTCCCTGCCTTCTC  
TGGGCTGTGCGGCCCCGAGTCTGCGTCCATTAGAGCACAGTCCACCCGAGGCTAGCACCGTGTCTGTGTCTGTCT  
CCCCCTCAGAGGAGCTCTCTCAAATGGGGATTAGCCTAACCCCACTCTGTCAACCACACCAGGATCGGGTGGGA  
CCTGGAGCTAGGGGGTGTGTTGCTGAGTGAGTGAGTGAAACACAGAATATGGGAATGGCAGCTGCTGAACCTGAAC  
CCAGAGCCTTCAGGTGCCAAAGCCATACTCAGGCCCCCAACGACATTGTCCACCTGGCCAGAAGGGTGCATGCC  
AATGGCAGAGACCTGGGATGGGAGAAGTCTGGGGCGCCAGGGGATCCAGCCTAGAGCAGACCTTAGCCCCCTGAC  
TAAGGCCTCAGACTAGGGCGGGAGGGGTCTCCTCCTCTCTGCTGCCAGTCTGGCCCCCTGCACAAGACAACAGA  
ATCCATCAGGGCCATGAGTGTCAACCAGACCTGACCCTACCAATTCCAGCCCCCTGACCCTCAGGACGCTGGATG  
CCAGCTCCAGCCCCAGTGCCGGGTCTCCTCCTCCTTCTGGCTTGGGGAGACCAGTTTCTGGGGAGCTTCCAAG  
AGCACCCACCAAGACACAGCAGGACAGGCCAGGGGAGGGCATCTGGACCAGGGGCATCCGTGCGGGCTATTGTACA  
GAGAAAAGAAGAGACCCACCCACTCGGGCTGCAAAAGGTGAAAAGCACCAAGAGGTTTTTCAGATGGAAGTGAGAG  
GTGACAGTGTGCTGGCAGCCCTCACAGCCCTCGCTTGCTCTCCCTGCCGCCTCTGCCTGGGCTCCCACTTTGGCA  
GCACTTGAGGAGCCCTTCAACCCGCGCTGCACTGTAGGAGCCCCCTTCTGGGCTGGCCAAGGCCGGAGCCAGCT  
CCCTCAGCTTGCGGGGAGGTGCGGAGGGAGAGGGGCGGGCAGGAACCGGGGCTGCGCGCAGCGCTTGCGGGCCAG  
AGTGAGTTCGGGTGGGCGTGGGCTCGGCGGGGCCCCACTCAGAGCAGCTGGCCGGCCCCAGGCAGTGAGGGCCT  
TAGCACCTGGGCCAGCAGCTGCTGTGCTCGATTTCTCGCTGGGCCTTAGCTGCCTCCCCGCGGGGCGAGGGCTCGG  
GACCTGCAGCCCTCCATGCCTGACCCTCCCCCCCCACCCCCCGTGGGCTCCTGTGCGGCCGGAGCCTCCCCAAGGAG  
CGCCGCCCCCTGCTCCACAGCGCCAGTCCCATCGACCACCCAAGGGCTGAGGAGTGCGGGTGCACAGCGCGGGA  
CTGGCAGGCAGCTCCACCTGCTGCCCCAGTGCTGGATCCACTGGGTGAAGCCAGCTGGGCTCCTGAGTCTGGTGG  
GGACTTGAGAAACCTTTATGTCTAGCTAAGGGATTGTAAATACACCGATGGGCACTCTGTATCTAGCTCAAGGTT  
TGTAACACACCAATCAGCACCCCTGTGTCTAGCTCAGTGTTTGTGAATGCACCAATCCACACTCTGTATCTGGCT  
ACTCTGGTGGGGACTTGAGAAACCTTTGTGTCCACACTCTGTATCTAGCTAATCTAGTGGGGATGTGGAGAACCT  
TTGTGTCTAGCTCAGGGATCGTAAACGCACCAATCAGCACCCCTGTCAAACAGACCACTTGACTCTGTAAAAT  
GGACCAATCAGCAGGATGTGGGTGGGGCGAGACAAGAGAATAAAAGCAGGCTGCCTGAGCCAGCAGTGACAACCC  
CCCTCGGGTCCCCCTCCACGCGCTGGAAGCTTTGTTCTTTCGCTCTTTGCAATAAATCTTGCTACTGCCAAAA

## **FIGURE 12**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA79862

><subunit 1 of 1, 571 aa, 1 stop

><MW: 62282, pI: 5.56, NX(S/T): 1

MERAVRVESGVLVGVCLLACPATATGPEVAQPEVDTTLGRVRGRQVGVKGTDRLVNVFLG  
IPFAQPPLGPDRFSAPHPAQPWEGVRDASTAPPMCLQDVESMNSSRFVLNGKQQIFSVSEDC  
LVLNVYSPAIEVPAGSGRPVMVWVHGGALITGAATSYDGSALAAYGDVVVVTVQYRLGVLGFF  
STGDEHAPGNQGFLDVVAALRWVQENIAPFGGDLNCVTVFGGSAGGSIISGLVLSPPAAGLF  
HRAITQSGVITTPGIIDSHPWPLAQKIAN TLACSSSSPAEMVQCLQQKEGEELVLSKKLKNT  
IYPLTVDGTVFPKSPKELLKEKPFHSVPFLMGVNNHEFSWLI PRGWGLLDTMEQMSREDMLA  
ISTPVLTS LDVPPPEMMPTVIDEYLGSNSDAQAKCQAFQEFMGDVFINVPTVSFSRYLRDSGS  
PVFFYEFQHRPSSFAKIKPAWVKADHGAEGAFVFGGPFLMDESSRLAFPEATEEEKQLSLTM  
MAQWTHFARTGDPNSKALPPWPQFNQAEQYLEINPVPRAGQKFREAWMQFWSETLPSKIQQW  
HQQQKNRKAQEDL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-27

#### **Transmembrane domain:**

amino acids 226-245

#### **N-glycosylation site.**

amino acids 105-109

#### **N-myristoylation sites.**

amino acids 10-16, 49-55, 62-68, 86-92, 150-156, 155-161,  
162-168, 217-223, 227-233, 228-234, 232-238, 262-268, 357-363,  
461-467

#### **Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23

#### **Carboxylesterases type-B serine active site.**

amino acids 216-232



## **FIGURE 13**

**CATG**GAGCCTCTTGCAGCTTACCCGCTAAAATGTTCCGGGGCCAGAGCAAAGGTATTTGCAG  
TTTTGCTGTCTATAGTTCTATGCACAGTAACGCTATTTCTTCTACAACTAAAATTCCTCAA  
CCTAAAATCAACAGCTTTTATGCCTTTGAAGTGAAGGATGCAAAGGAAGAACTGTTTCTCT  
GGAAAAGTATAAAGGCAAAGTTTCACTAGTTGTAAACGTGGCCAGTGACTGCCAACTCACAG  
ACAGAAATTACTTAGGGCTGAAGGAACTGCACAAAGAGTTTGGACCATCCCCTTCAGCGTG  
TTGGCTTTTCCCTGCAATCAGTTTGGAGAATCGGAGCCCCGCCCAAGCAAGGAAGTAGAATC  
TTTTGCAAGAAAAAACTACGGAGTAACTTTCCCCATCTTCCACAAGATTAAGATTCTAGGAT  
CTGAAGGAGAACCTGCATTTAGATTTCTTGTTGATTCTTCAAAGAAGGAACCAAGGTGGAAT  
TTTTGGAAGTATCTTGTC AACCTGAGGGTCAAGTTGTGAAGTTCTGGAGGCCAGAGGAGCC  
CATTGAAGTCATCAGGCCTGACATAGCAGCTCTGGTTAGACAAGTGATCATAAAAAAGAAAG  
AGGATCTA**TGA**GAATGCCATTGCGTTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTTG  
GTCTCATTTTAAACATTTTTTTTTTTGGAGACAGTGTCTCACTCTGTCACCCAGGCTGGAGTG  
CAGTAGTGCGTTCTCAGCTCATTGCAACCTCTGCCTTTTTTAAACATGCTATTAAATGTGGCA  
ATGAAGGATTTTTTTTTTAAATGTTATCTTGCTATTAAGTGGTAATGAATGTTCCCAGGATGAG  
GATGTTACCCAAAGCAAAAATCAAGAGTAGCCAAAGAATCAACATGAAATATATTA ACTACT  
TCCTCTGACCATACTAAAGAATTCAGAATACACAGTGACCAATGTGCCTCAATATCTTATTG  
TTCAACTTGACATTTTCTAGGACTGTACTTGATGAAAATGCCAACACACTAGACCACTCTTT  
GGATTCAAGAGCACTGTGTATGACTGAAATTTCTGGAATAACTGTAAATGGTTATGTTAATG  
GAATAAAACACAAATGTTGAAAAATGTAAAATATATATACATAGATTCAAATCCTTATATAT  
GTATGCTTGTTTTGTGTACAGGATTTTGTTTTTTCTTTTTTAAGTACAGGTTCCTAGTGTTTT  
ACTATAACTGTC ACTATGTATGTA ACTGACATATATAAATAGTCATTTATAAATGACCGTAT  
TATAACATTTGAAAAAGTCTTCATCAAAAAAAAAAAAAAAAAA

## **FIGURE 14**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80136

><subunit 1 of 1, 209 aa, 1 stop

><MW: 23909, pI: 9.68, NX(S/T): 0

MEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQLKFLKPKINSFYAFEVKDAKGRTVSL  
EKYKGKVSLLVNVASDCQLTDRNYLGLKELHKEFGPSHFSLAFPCNQFGESEPRPSKEVES  
FARKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWKYLVNPEGQVVKFWRPEEP  
IEVIRPDIAALVRQVVIKKKEDL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-31

#### **Glutathione peroxidases signature 2.**

amino acids 104-112

#### **Glutathione peroxidases.**

amino acids 57-82

## FIGURE 15

TGTCGCCTGGCCCTCGCC**ATG**CAGACCCCGCGAGCGTCCCCTCCCCGCCCGGCCCTCCTGCTTCTGCTGCTGCTA  
CTGGGGGGCGCCACGGCCCTCTTTCCTGAGGAGCCGCGCCGCTTAGCGTGGCCCCCAGGGACTACCTGAACCAC  
TATCCCGTGTTTGTGGGCAGCGGGCCCGGACGCCTGACCCCGCAGAAGGTGCTGACGACCTCAACATCCAGCGA  
GTCCTGCGGGTCAACAGGACGCTGTTTATTGGGGACAGGGACAACCTCTACCGCGTAGAGCTGGAGCCCCCACC  
TCCACGGAGCTGCGGTACCAGAGGAAGCTGACCTGGAGATCTAACCCAGCGACATAAACGTGTGTGCGGATGAAG  
GGCAAACAGGAGGGCGAGTGTGCAAACTTCGTAAAGGTGCTGCTCCTTCGGGACGAGTCCACGCTCTTTGTGTGC  
GGTTCCAACGCCTTCAACCCGGTGTGCGCCAACTACAGCATAGACACCCTGCAGCCCGTCGGAGACAACATCAGC  
GGTATGGCCCGCTGCCCCGTACGACCCCAAGCACGCCTAATGTTGCCCTCTTCTCTGACGGGATGCTCTTCACAGCT  
ACTGTTACCGACTTCCTAGCCATTGATGCTGTCTATCTACCGCAGCCTCGGGGACAGGGCCACCCTGCGCACCGTG  
AAACATGACTCCAAGTGGTTCAAAGAGCCTTACTTTGTCCATGCGGTGGAGTGGGGCAGCCATGTCTACTTCTTC  
TTCCGGGAGATTGCGATGGAGTTTAACTACCTGGAGAAGGTGGTGGTGTCCCGCGTGGCCCCGAGTGTGCAAGAAC  
GACGTGGGAGGCTCCCCCGCGTGTGGAGAAGCAGTGGACGCTCCTTCTGAAGGCGCGGCTCAACTGCTCTGTA  
CCCGGAGACTCCCATTTCTACTTCAACGTGCTGCAGGCTGTACGGGCGTGGTCAGCCTCGGGGGCCGGCCCGTG  
GTCCTGGCCGTTTTTTCCACGCCCAGCAACAGCATCCCTGGCTCGGCTGTCTGCGCCTTTGACCTGACACAGGTG  
GCAGCTGTGTTTGAAGGCCGCTTCCGAGAGCAGAAGTCCCCCGAGTCCATCTGGACGCCGGTGCCGGAGGATCAG  
GTGCCTCGACCCCGGCCCGGGTGTGCGCAGCCCCCGGGATGCAGTACAATGCCTCCAGCGCCTTGCCGGATGAC  
ATCCTCAACTTTGTCAAGACCCACCCTCTGATGGACGAGGCGGTGCCCTCGCTGGGCCATGCGCCCTGGATCCTG  
CGGACCCTGATGAGGCACCAGCTGACTCGAGTGGCTGTGGACGTGGGAGCCGGCCCCCTGGGGCAACCAGACCGTT  
GTCTTCTGGGTTCTGAGGCGGGGACGGTCTCAAGTTCTCGTCCGGCCCAATGCCAGCACCTCAGGGACGTCT  
GGGCTCAGTGTCTTCTGGAGGAGTTTGAGACCTACCGGCCGACAGGTGTGGACGGCCCCGGCGGTGGCGAGACA  
GGGCAGCGGCTGCTGAGCTTGGAGCTGGACGCAGCTTCGGGGGGCCTGCTGGCTGCCTTCCCCGCTGCGTGGTC  
CGAGTGCCTGTGGCTCGCTGCCAGCAGTACTCGGGGTGTATGAAGAACTGTATCGGCAGTCAGGACCCCTACTGC  
GGGTGGGCCCCCGACGGCTCCTGCATCTTCTCAGCCCCGGGCACCAGAGCCGCCTTTGAGCAGGACGTGTCCGGG  
GCCAGCACCTCAGGCTTAGGGGACTGCACAGGACTCCTGCGGGCCAGCCTCTCCGAGGACCGCGCGGGGCTGGTG  
TCGGTGAACCTGCTGGTAACGTCGTCGGTGGCGGCCTTCGTGGTGGGAGCCGTGGTGTCCGGCTTCAGCGTGGGC  
TGGTTCTGTGGGCTCCGTGAGCGGCGGGAGCTGGCCCCGCGCAAGGACAAGGAGGCCATCCTGGCGCACGGGGCG  
GGCGAGGCGGTGCTGAGCGTCAGCCGCCTGGGCGAGCGCAGGGCGCAGGGTCCCGGGGGCCGGGGCGGAGGCGGT  
GGCGGTGGCGCCGGGGTTCCCCCGGAGGCCCTGCTGGCGCCCTGATGCAGAACGGCTGGGCCAAGGCCACGCTG  
CTGCAGGGCGGGCCCCACGACCTGGACTCGGGGCTGCTGCCACGCCGAGCAGACGCCGCTGCCGCAAGCGC  
CTGCCACTCCGCACCCGCACCCCCACGCCCTGGGCCCCCGCGCCTGGGACCACGGCCACCCCCCTGCTCCCGGCC  
TCCGCTTCATCCTCCCTCCTGCTGCTGGCGCCCGCCGGGCCCGGAGCAGCCCCCGCGCCTGGGGAGCCGACC  
CCCGACGGCCGCCTCTATGCTGCCCGGCCCGGCCGCGCCTCCACGGCGACTTCCCGCTACCCCCCACGCCAGC  
CCGGACCGCCGGCGGGTGGTGTCCGCGCCACGGGCCCTTGGACCCAGCCTCAGCCGCCGATGGCCTCCCGCGG  
CCCTGGAGCCCGCCCCCGACGGGCAGCCTGAGGAGGCCACTGGGCCCCCACGCCCTCCGGCCGCCACCCTGCGC  
CGCACCCACACGTTCAACAGCGGCGAGGCCCGGCCCTGGGGACCGCCACCGCGGCTGCCACGCCCGGGCGGGCACA  
GACTTGGCCACCTCCTCCCCATGAGGGGGCGGACAGGACTGCGCCCCCGTGCCCT**TAG**CGCGGGGGCCCCCG  
ATGCCTTGGCAGTGCCAGCCACGGGAACCAGGAGCGAGAGACGGTGCCAGAAGCCGGGGCCCGGGGCAACTCCG  
AGTGGGTGCTCAAGTCCCCCGCGACCCACCCGCGGAGTGGGGGGCCCCCTCCGCCACAAGGAAGCACAACCAG  
CTCGCCCTCCCCCTACCCGGGGCCGAGGACGCTGAGACGGTTTGGGGGTGGGTGGGCGGGAGGACTTTGCTATG  
GATTTGAGGTTGACCTTATGCGCGTAGGTTTTGGTTTTTTTTTGCAGTTTTGGTTTTCTTTTGCGGTTTTCTAACC  
AATTGCACAACTCCGTTCTCGGGGTGGCGGCAGGAGGGGAGGCTTGGACGCCGGTGGGGAATGGGGGGCCACAG  
CTGCAGACCTAAGCCCTCCCCACCCCTGGAAAGGTCCCTCCCCAACCCAGGCCCTGGCGTGTGTGGGTGTGCG  
TGCGTGTGCGTGCCGTGTTCTGTGTGCAAGGGGCGGGGAGGTGGGCGTGTGTGTGCGTGCCAGCGAAGGCTGCTG  
TGGGCGTGTGTGTCAAGTGGGCCACGCGTGAGGGTGTGTGTCCACGAGCGACGATCGTGGTGGCCCCAGCGGCC  
TGGGCGTTGGCTGAGCCGACGCTGGGGCTTCCAGAAGGCCCGGGGGTCTCCGAGGTGCCGGTTAGGAGTTTGAAC  
CCCCCCCCACTCTGCAGAGGGAAGCGGGGACAATGCCGGGGTTTCAGGCAGGAGACACGAGGAGGGCCTGCCCGGA  
AGTCACATCGGCAGCAGCTGTCTAAAGGGCTTGGGGGCCTGGGGGGCGGCGAAGGTGGGTGGGGCCCCCTCTGTAA  
ATACGGCCCCAGGGTGGTGAGAGAGTCCCATGCCACCCGTCCCTTGTGACCTCCCCCTATGACCTCCAGCTGA  
CCATGCATGCCACGTGGCTGGCTGGGTCTCTGCCCTCTTTGGAGTTTGCCTCCCCCAGCCCCCTCCCCATCAAT  
AAACTCTGTTTACAACCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

## FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80145

><subunit 1 of 1, 888 aa, 1 stop

><MW: 95285, pI: 8.89, NX(S/T): 8

MQTPRASPPRPALLLLLLLLLLLGGAHGLFPEEPPLSVAPRDYLNHYPVFVVGSGPGRLTPAEGA  
DDLNIQVRVLRVNRTLFIGDRDNLYRVELEPPTSTELRYQRKLTWRSNPSDINVCRMKGKQEG  
ECRNFKVLLLRDESTLFVCGSNAFNPVCANYSIDTLQPVGDNISGMARCPYDPKHANVALF  
SDGMLFTATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWFKEPYFVHAVEWGS HVYFFFREI  
AMEFNYLEKVVVSRVARVCKNDVGGSPRVLEKQWTSFLKARLNCSVPGDSHFYFNVLQAVTG  
VVSLGGRPVVLAVFSTPSNSIPGSAVCAFDLTQVAAVFEGRFREQKSPESIWTVPEDQVPR  
PRPGCCAAPGMQYNASSALPDDILNFVKTHPLMDEAVPSLGHAPWILRTLMRHQLTRVAVDV  
GAGPWGNQTVVFLGSEAGTVLKFVLRPNASTSGTSGLSVFLEEFETYRPDRCGRPGGGETGQ  
RLLSLELDAASGGLLA AFPRCVVRVPVARCQQYSGCMKNCIGSQDPYCGWAPDGSCIFLSPG  
TRAAFEQDVSGASTSGLGDC TGLLRASLSEDRAGLVSVNLLVTSSVAAFVVGAVVSGFSVGW  
FVGLRERRELARRKDKEAILAHGAGEAVLSVSRLGERRAQGPGRGGGGGGGAGVPPEALLA  
PLMQNGWAKATLLQGGPHDLDSGLLPTPEQTPLPQKRLPTPHPHPHALGPRAWDHGHPLLP  
SASSSLLLLAPARAPEQPPAPGEPTPDGRLYAARPGRASHGDFPLTPHASPD RRRRVVSAPTG  
PLDPASAADGLPRPWSPPTGSLRRPLGPHAPPAATLRRTHTFNSGEARPGDRHRGCHARPG  
TDLAHL LPYGGADRTAPPVP

### Important features of the protein:

#### Signal peptide:

amino acids 1-25

#### Transmembrane domains:

amino acids 318-339, 598-617

#### N-glycosylation sites.

amino acids 74-78, 155-159, 167-171, 291-295, 386-390, 441-445,  
462-466

#### Glycosaminoglycan attachment sites.

amino acids 51-55, 573-577

#### cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

#### N-myristoylation sites.

amino acids 21-27, 50-56, 189-195, 333-339, 382-388, 448-454,  
490-496, 491-497, 508-514, 509-515, 531-537, 558-564, 569-575,  
574-580, 580-586, 610-616, 643-649, 663-669, 666-672, 667-673,  
668-674, 669-675, 670-676, 868-874, 879-885



## FIGURE 17

AGCAACTCAAGTTCATCATTGTCCTGAGAGAGAGGAGCAGCGCGGTTCCTCGGCCGGGACAGC  
AGAACGCCAGGGGACCCTCACCTGGGCGCGCCGGGGCACGGGCTTTGATTGTCCTGGGGTCG  
CGGAGACCCGCGCGCCTGCCCTGCACGCCGGGCGGCAACCTTTGCAGTCGCGTTGGCTGCTG  
CGATCGGCCGGCGGGTCCCTGCCGAAGGCTCGGCTGCTTCTGTCCACCTCTTACACTTCTTC  
ATTTATCGGTGGATCATTTTCGAGAGTCCGTCTTGTAATGTTTGGCACTTTGCTACTTTATT  
GCTTCTTTCTGGCGACAGTTCCAGCACTCGCCGAGACCGGCGGAGAAAGGCAGCTGAGCCCG  
GAGAAGAGCGAAATATGGGGACCCGGGCTAAAAGCAGACGTCGTCCTTCCCGCCCGCTATTT  
CTATATTCAGGCAGTGGATACATCAGGGAATAAATTCACATCTTCTCCAGGCGAAAAGGTCT  
TCCAGGTGAAAGTCTCAGCACCAGAGGAGCAATTCACTAGAGTTGGAGTCCAGGTTTTAGAC  
CGAAAAGATGGGTCCTTCATAGTAAGATACAGAATGTATGCAAGCTACAAAAATCTGAAGGT  
GGAAATTAAATTCCAAGGGCAACATGTGGCCAAATCCCCATATATTTTAAAAGGGCCGGTTT  
ACCATGAGAACTGTGACTGTCCTCTGCAAGATAGTGCAGCCTGGCTACGGGAGATGAACTGC  
CCTGAAACCATTGCTCAGATTCAGAGAGATCTGGCACATTTCCCTGCTGTGGATCCAGAAAA  
GATTGCAGTAGAAATCCCAAAAAGATTTGGACAGAGGCAGAGCCTATGTCACTACACCTTAA  
AGGATAACAAGGTTTATATCAAGACTCATGGTGAACATGTAGGTTTTAGAATTTTCATGGAT  
GCCATACTACTTTCTTTGACTAGAAAGGTGAAGATGCCAGATGTGGAGCTCTTTGTTAATTT  
GGGAGACTGGCCTTTGGAAAAAAGAAATCCAATTCAAACATCCATCCGATCTTTTCCTGGT  
GTGGCTCCACAGATTCCAAGGATATCGTGATGCCTACGTACGATTTGACTGATTCTGTTCTG  
GAAACCATGGGCCGGGTAAGTCTGGATATGATGTCCGTGCAAGCTAACACGGGTCCTCCCTG  
GGAAAGCAAAAATTCCACTGCCGTCTGGAGAGGGCGAGACAGCCGCAAAGAGAGACTCGAGC  
TGGTTAAACTCAGTAGAAAACACCCAGAACTCATAGACGCTGCTTTCACCAACTTTTTCTTC  
TTTAAACACGATGAAAACCTGTATGGTCCCATTTGTGAAACATATTTTCATTTTTTGATTTCTT  
CAAGCATAAGTATCAAATAAATATCGATGGCACTGTAGCAGCTTATCGCCTGCCATATTTGC  
TAGTTGGTGACAGTGTTGTGCTGAAGCAGGATTCCATCTACTATGAACATTTTTTACAATGAG  
CTGCAGCCCTGGAAACACTACATTCCAGTTAAGAGCAACCTGAGCGATCTGCTAGAAAAACT  
TAAATGGGCGAAAGATCACGATGAAGAGGCCAAAAAGATAGCAAAAGCAGGACAAGAATTTG  
CAAGAAATAATCTCATGGGCGATGACATATTCTGTTATTATTTCAAACCTTTTCCAGGAATAT  
GCCAATTTACAAGTGAGTGAGCCCCAAATCCGAGAGGGCATGAAAAGGGTAGAACCACAGAC  
TGAGGACGACCTCTTCCCTTGTAATTGCCATAGGAAAAAGACCAAAGATGAACTCTGATATG  
CAAAATAACTTCTATTAGAATAATGGTGCTCTGAAGACTCTTCTTAATAAAAAGAAGAATT  
TTTTTAAGTATTAATTCCATGGACAATATAAAATCTGTGTGATTGTTTGCAGTATGAAGACA  
CATTTCTACTTATGCAGTATTCTCATGACTGTACTTTAAAGTACATTTTTTAGAATTTTATAA  
TAAACACCTTTATTTTAAAGGAAAAAAA

## **FIGURE 18**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84917

><subunit 1 of 1, 502 aa, 1 stop

><MW: 58043, pI: 7.94, NX(S/T): 2

MFGTLLLYCFFLATVPALAETGGERQLSPEKSEIWGPGLKADVVLPAFYFYIQAVDTSGNKF  
TSSPGEKVFQVKVSAPEEQFTRVGVQVLDRKDGSFIVRYRMYASYKNLKVEIKFQGQHVAKS  
PYILKGPVYHENCDCPLQDSAAWLREMNCPETIAQIQRDLAHFPAVDPEKIAVEIPKRFGQR  
QSLCHYTLKDNKVYIKTHGEHVGFRIFMDAILLSLTRKVKMPDVELFVNLGDWPLEKKKSNS  
NIHPIFSWCGSTDSKDIVMPTYDLTDSVLETMGRVSLDMMSVQANTGPPWESKNSTAVWRGR  
DSRKERLELVKLSRKHPOLIDAAFTNFFFFKHDENLYGPIVKHISFFDFFKHKYQINIDGTV  
AAYRLPYLLVGDSVVLKQDSIYYEHFYNELQPWKHYIPVKSNSDLLEKLKWAKDHDEEAKK  
IAKAGQEFARNNLMGDDIFCYFCLKFQEYANLQVSEPQIREGMKRVEPQTEDDLFPCTCHRK  
KTKDEL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-17

#### **N-glycosylation sites.**

amino acids 302-306, 414-418

#### **cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 243-247, 495-499

#### **Tyrosine kinase phosphorylation site.**

amino acids 341-348

#### **N-myristoylation sites.**

amino acids 59-65, 118-124, 184-190, 258-264, 370-376, 439-445

#### **Endoplasmic reticulum targeting sequence.**

amino acids 499-504

## FIGURE 19

CCTGGAGCCGGAAGCGCGGCTGCAGCAGGGCGAGGCTCCAGGTGGGGTCGGTTCCGCATCCA  
GCCTAGCGTGTCACG**ATG**CGGCTGGGCTCCGGGACTTTCGCTACCTGTTGCGTAGCGATCG  
AGGTGCTAGGGATCGCGGTCTTCCTTCGGGGATTCTTCCCGGCTCCCGTTTCGTTCTCTGCC  
AGAGCGGAACACGGAGCGGAGCCCCCAGCGCCCGAACCCTCGGCTGGAGCCAGTTCTAACTG  
GACCACGCTGCCACCACCTCTCTTCAGTAAAGTTGTTATTGTTCTGATAGATGCCTTGAGAG  
ATGATTTTGTGTTTGGGTCAAAGGGTGTGAAATTTATGCCCTACACAACCTTACCTTGTGGAA  
AAAGGAGCATCTCACAGTTTTGTGGCTGAAGCAAAGCCACCTACAGTTACTATGCCTCGAAT  
CAAGGCATTGATGACGGGGAGCCTTCCTGGCTTTGTGCGACGTCATCAGGAACCTCAATTCTC  
CTGCACTGCTGGAAGACAGTGTGATAAGACAAGCAAAAGCAGCTGGAAAAAGAATAGTCTTT  
TATGGAGATGAAACCTGGGTAAATTATTCCCAAAGCATTTTGTGGAATATGATGGAACAAC  
CTCATTTTTTCGTGTCAGATTACACAGAGGTGGATAATAATGTCACGAGGCATTTGGATAAAG  
TATTA AAAAGAGGAGATTGGGACATATTAATCCTCCACTACCTGGGGCTGGACCACATTGGC  
CACATTT CAGGGCCCAACAGCCCCCTGATTGGGCAGAAGCTGAGCGAGATGGACAGCGTGCT  
GATGAAGATCCACACCTCACTGCAGTCGAAGGAGAGAGAGACGCCTTTACCCAATTTGCTGG  
TTCTTTGTGGTGACCATGGCATGTCTGAAACAGGAAGTCACGGGGCCTCCTCCACCGAGGAG  
GTGAATACACCTCTGATTTTAATCAGTTCTGCGTTTGAAAGGAAACCCGGTGATATCCGACA  
TCCAAAGCACGTCCAAT**TAG**ACGGATGTGGCTGCGACACTGGCGATAGCACTTGGCTTACCGA  
TTCCAAAAGACAGTGTAGGGAGCCTCCTATTCCCAGTTGTGGAAGGAAGACCAATGAGAGAG  
CAGTTGAGATTTTACATTTGAATACAGTGCAGCTTAGTAAACTGTTGCAAGAGAATGTGCC  
GTCATATGAAAAAGATCCTGGGTTTGAGCAGTTTAAATGTCAGAAAGATTGCATGGGAACCT  
GGATCAGACTGTACTTGGAGGAAAAGCATTCAGAAGTCCTATTCAACCTGGGCTCCAAGGTT  
CTCAGGCAGTACCTGGATGCTCTGAAGACGCTGAGCTTGTCCTGAGTGCACAAGTGGCCCA  
GTTCTCACCTTGCTCCTGCTCAGCGTCCCACAGGCCTGCACAGAAAGGCTGAGCTGGAAGT  
CCCCTGTCATCTCCTGGGTTTTCTCTGCTCTTTTATTTGGTGATCCTGGTTCTTTTCGGCCG  
TTCACGTCATTGTGTGCACCTCAGCTGAAAGTTTCGTGCTACTTCTGTGGCCTCTCGTGGCTG  
GCGGCAGGCTGCCTTTTCGTTTACCAGACTCTGGTTGAACACCTGGTGTGTGCCAAGTGCTGG  
CAGTGCCCTGGACAGGGGGCCTCAGGGAAGGACGTGGAGCAGCCTTATCCCAGGCCTCTGGG  
TGTCCCGACACAGGTGTTACATCTGTGCTGTCAGGTCAGATGCCTCAGTTCTTGAAAGCT  
AGGTTCCCTGCGACTGTTACCAAGGTGATTGTAAAGAGCTGGCGGTACAGAGGAACAAGCCC  
CCCAGCTGAGGGGGTGTGTGAATCGGACAGCCTCCCAGCAGAGGTGTGGGAGCTGCAGCTGA  
GGGAAGAAGAGACAATCGGCCTGGACACTCAGGAGGGTCAAAGGAGACTTGGTCGCACCAC  
TCATCCTGCCACCCCCAGAATGCATCCTGCCTCATCAGGTCCAGATTTCTTTCCAAGGCGGA  
CGTTTTCTGTTGGAATTCTTAGTCCTTGGCCTCGGACACCTTCATTCGTTAGCTGGGGAGTG  
GTGGTGAGGCAGTGAAGAAGAGGCGGATGGTCACACTCAGATCCACAGAGCCCAGGATCAAG  
GGACCCACTGCAGTGGCAGCAGGACTGTTGGGCCCCCACCCTGCACAGCCCTCATC  
CCCTCTTGGCTTGAGCCGTCAGAGGCCCTGTGCTGAGTGTCTGACCGAGACACTCACAGCTT  
TGTCATCAGGGCACAGGCTTCCTCGGAGCCAGGATGATCTGTGCCACGCTTGACCTCGGGC  
CCATCTGGGCTCATGCTCTCTCTCCTGCTATTGAATTAGTACCTAGCTGCACACAGTATGTA  
GTTACCAAAGAATAAACGGCAATAATTGAGAAAAAAA

## **FIGURE 20**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84920

><subunit 1 of 1, 310 aa, 1 stop

><MW: 33875, pI: 7.08, NX(S/T): 2

MRLGSGTFATCCVAIEVLGIAVFLRGFFPAPVRSSARAEHGAEPPEPSAGASSNWTTLPP  
PLFSKVIVLIDALRDDFVFGSKGVKFMPYTTYLVEKGASHSFVAEAKPPTVTMPRIKALMT  
GSLPGFVDVIRNLNSPALLEDVIRQAKAAGKRIVFYGDETWWKLFPKHFEYDGTTSFFVS  
DYTEVDNNVTRHLDKVLKRGDWDILILHYLGLDGHIGHISGPNSPLIGQKLSEMDSVLMKIHT  
SLQSKERETPLPNLLVLCGDHGMSETGSHGASSTEEVNTPLILISSAFERKPGDIRHPKHVQ

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-34

#### **Transmembrane domain:**

amino acids 58-76

#### **N-glycosylation sites.**

amino acids 56-60, 194-198

#### **N-myristoylation sites.**

amino acids 6-12, 52-58, 100-106, 125-131, 233-239, 270-276,  
275-281, 278-284

#### **Amidation site.**

amino acids 154-158

#### **Cell attachment sequence.**

amino acids 205-208

## **FIGURE 21**

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCA**ATG**GCAAT  
GGGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCC  
AAGCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCTTTGACCTCAGGGCCATG  
AAGCTGCCCAGCATCTCCTGTCCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGG  
GTATCGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGCCAGA  
CGCAATCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACCTGAC  
AAATGCAACGCCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCC  
GCCGACGCTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTA  
TCGGCAGGTCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGC  
AGAATGACAGTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTG  
CACCACCGAGGGCACCACCAGCCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGG  
GGTACCTCTGCAACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCT  
CCCCGAGCACTACAGGTCCTGGCCCTGCTCCTCCCAGTCCTCCTGCTGGTGGGGCTCTCAGC  
**ATAG**ACCGCCCCCTCCAGGATGCTGGGGACAGGGCTCACACACCTCATTCTTGCTGCTTCAGC  
CCCTATCACATAGCTCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

## **FIGURE 22**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576

><subunit 1 of 1, 251 aa, 1 stop

><MW: 26935, pI: 7.42, NX(S/T): 2

MAMGVPRVILLCLFGAALCLTGSQALQCYSEHTYFGPFDLRAMKLPSISCPHECFEAILSL  
DTGYRAPVTLVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNAHLMTHDALPNLSQA  
PDPPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQSGRMTVGNFSVPVYIRTCHR  
PSCTTEGTTSPWTAIDLQSCCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVGLSA

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-19

#### **Transmembrane domain:**

amino acids 233-251

#### **N-glycosylation sites.**

amino acids 120-124, 174-178

#### **N-myristoylation sites.**

amino acids 15-21, 84-90



## FIGURE 23

CCCACGCGTCCGGGACAGATGAACTTAAAAGAGAAGCTTTAGCTGCCAAAGATTGGGAAAGG  
GAAAGGACAAAAAAGACCCCTGGGCTACACGGCGTAGGTGCAGGGTTTCCTACTGCTGTTCT  
TTTATGCTGGGAGCTGTGGCTGTAACCAACTAGGAAATAACGTATGCAGCAGCT**ATGG**CTGT  
CAGAGAGTTGTGCTTCCCAAGACAAAGGCAAGTCCTGTTTCTTTTTCTTTTTTGGGGAGTGT  
CCTTGGCAGGTTCTGGGTTTGGACGTTATTCGGTGACTGAGGAAACAGAGAAAGGATCCTTT  
GTGGTCAATCTGGCAAAGGATCTGGGACTAGCAGAGGGGGAGCTGGCTGCAAGGGGAACCAG  
GGTGGTTTCCGATGATAACAAACAATACCTGCTCCTGGATTACATACCGGGAATTTGCTCA  
CAAATGAGAACTGGACCGAGAGAAGCTGTGTGGCCCTAAAGAGCCCTGTATGCTGTATTTTC  
CAAATTTTAATGGATGATCCCTTTTTCAGATTTACCGGGCTGAGCTGAGAGTCAGGGATATAAA  
TGATCACGCGCCAGTATTTTCAGGACAAAGAAACAGTCTTAAAAATATCAGAAAATACAGCTG  
AAGGGACAGCATTTAGACTAGAAAGAGCACAGGATCCAGATGGAGGACTTAACGGTATCCAA  
AACTACACGATCAGCCCCAACTCTTTTTTCCATATTAACATTAGTGGCGGTGATGAAGGCAT  
GATATATCCAGAGCTAGTGTTGGACAAAGCACTGGATCGGGAGGAGCAGGGAGAGCTCAGCT  
TAACCCTCACAGCGCTGGATGGTGGGTCTCCATCCAGGTCTGGGACCTCTACTGTACGCATC  
GTTGTCTTGGACGTCAATGACAATGCCCCACAGTTTGCCCAGGCTCTGTATGAGACCCAGGC  
TCCAGAAAACAGCCCCATTGGGTTCCTTATTGTTAAGGTATGGGCAGAAGATGTAGACTCTG  
GAGTCAACGCGGAAGTATCCTATTCATTTTTTTGATGCCTCAGAAAATATTCGAACGACCTTT  
CAAATCAATCCTTTTTTCTGGGGAAATCTTCTCAGAGAATTGCTTGATTATGAGTTAGTAAA  
TTCTTACAAAATAAATATACAGGCAATGGACGGTGGAGGCCTTTCTGCAAGATGTAGGGTTT  
TAGTGGAAGTATTGGACACCAATGACAATCCCCCTGAACTGATCGTATCATCATTTTTCCAAC  
TCTGTTGCTGAGAATTCTCCTGAGACGCCGCTGGCTGTTTTTAAGATTAATGACAGAGACTC  
TGGAGAAAATGGAAAGATGGTTTGCTACATTCAAGAGAATCTGCCATTCTACTAAAACCTT  
CTGTGGAGAATTTTTTACATCCTAATTACAGAAGGCGCGCTGGACAGAGAGATCAGAGCCGAG  
TACAACATCACTATCACCGTCACTGACTTGGGGACACCCAGGCTGAAAACCGAGCACAAACAT  
AACGGTCCTGGTCTCCGACGTCAATGACAACGCCCCCGCCTTCACCCAAACCTCCTACACCC  
TGTTTCGTCCGCGAGAACAACAGCCCCGCCCCTGCACATCGGCAGCGTCAGCGCCACAGACAGA  
GACTCGGGCACCAACGCCCAGGTCACCTACTCGCTGCTGCCGCCCAAGACCCGCGACCTGCC  
CCTCGCCTCCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTTCGCCCTCAGGTGCTGG  
ACTACGAGGCCCTGCAGGCTTTCGAGTTCCGCGTGCGGCCACAGACCGCGGCTCCCCCGCG  
CTGAGCAGAGAGGCGCTGGTGGCGGTGCTGGTGCTGGACGCCAACGACAACCTCGCCCTTCGT  
GCTGTACCCGCTGCAGAACGGCTCCGCGCCCTGCACCGAGCTGGTGCCCCGGGCGGCCGAGC  
CGGGCTACCTGGTGACCAAGGTGGTGGCGGTGGACGGCGACTCGGGCCAGAACGCCTGGCTG  
TCGTACCAGCTGCTCAAGGCCACGGAGCCCGGGCTGTTCCGGTGTGTGGGCGCACAAATGGGGA  
GGTGCGCACCGCCAGGCTGCTGAGCGAGCGCGACGCAGCCAAGCACAGGCTCGTGGTGCTTG  
TCAAGGACAATGGCGAGCCTCCTCGCTCGGCCACCGCCACGCTGCACTTGCTCCTGGTGGAC  
GGCTTCTCCAGCCCTACCTGCCTCTCCCGGAGGCGGCCCGGGCCAGGCCAGGCCGAGGC  
CGACTTGCTCACCGTCTACCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCCTCCTCT  
CGGTGCTCCTGTTTCGTGGCGGTGCGGCTGTGCAGGAGGAGCAGGGCGGCCTCGGTGGGTGCG  
TGCTCGGTGCCCGAGGGTCTTTTTCCAGGGCATCTGGTGGACGTGAGGGGCGCTGAGACCCT  
GTCCAGAGCTACCAGTATGAGGTGTGTCTGACGGGAGGCCCGGGACCAGTGAGTTCAAGT  
TCTTGAAACCAGTTATTTTCGGATATTCAGGCACAGGGCCCTGGGAGGAAGGGTGAAGAAAAT  
TCCACCTTCCGAAATAGCTTTGGATTTAATATTCAG**TAA**AGTCTGTTTTTAGTTTTCATATAC  
TTTTGGTGTGTTACATAGCCATGTTTCTATTAGTTTACTTTTAAATCTCAAATTTAAGTTAT  
TATGCAACTTCAAGCATTATTTTCAAGTAGTATACCCCTGTGGTTTTTACAATGTTTCATCAT  
TTTTTTGCATTAATAACAACCTGGGTTTTAATTTAATGAGTATTTTTTTCTAAATGATAGTGT  
AAGGTTTTAATTCTTTCCAACCTGCCCAAGGAATTAATTACTATTATATCTCATTACAGAAAT  
CTGAGGTTTTGATTCATTTTCAGAGCTTGCACTCATGATTCTAATCACTTCTGTCTATAGTG  
TACTTGCTCTATTTAAGAAGGCATATCTACATTTCCAAACTCATTCTAACATTTCTATATATT  
CGTGTTTGAAAACCATGTCATTTATTTCTACATCATGTATTTAAAAAGAAATATTTCTCTAC  
TACTATGCTCATGACAAAATGAAACAAAGCATATTGTGAGCAATACTGAACATCAATAATAC  
CCTTAGTTTATATACTTATTATTTTATCTTTAAGCATGCTACTTTTACTTGGCCAATATTTT  
CTTATGTAACTTTTGCTGATGTATAAAACAGACTATGCCTTATAATTGAAATAAAATTATA  
ATCTGCCTGAAAATGAATAAAAATAAAACATTTTGAAATGTGAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 24**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA87976

><subunit 1 of 1, 800 aa, 1 stop

><MW: 87621, pI: 4.77, NX(S/T): 7

MAVRELCFPRQRQVLFLFLFWGVSLAGSGFGRYSVTEETEKGSFVVNLAKDLGLAEGELAAR  
GTRVVSDDNKQYLLLDSTGNLLTNEKLDREKLCGPKEPCMLYFQILMDDPFQIYRAELRVR  
DINDHAPVFQDKETVLKISENTAEGTAFRLERAQDPDGGNLGIQNYTISPNSFFHINISGGD  
EGMIYPELVLDKALDREEQGELSLLTALDGGSPSRSGTSTVRIVVLDVNDNAPQFAQALYE  
TQAPENSPIGFLIVKVWAEVDVSGVNAEVSYSFFDASENIRTTFQINPFSGEIFLRELLDYE  
LVNSYKINIQAMDGGGLSARCRVLVEVLDTNDNPPELIVSSFSNSVAENSPETPLAVFKIND  
RDSGENGMVCYIQENLPFLKPSVENFYILITEGALDREIRAENITITVTDLGTPRLKTE  
HNITVLVSDVNDNAPAFQTQTSYTLFVRENNSPALHIGSVSATDRDSGTNAQVTYSLLPPQDP  
HLPLASLV SINADNGHLFALRSLDYEALQAFEFVRVGATDRGSPALSREALVRVLVLDANDNS  
PFVLYPLQNGSAPCTELVPRAAEPGYLVTKVVAVDGDGSGQNAWLSYQLLKATEPGLFGVWAH  
NGEVRTARLLSERDAAKHRLVVLVKDNGEPPRSATATLHLLLVDGFSQPYLPLPEAAPAQAAQ  
AEADLLTVYLVVALASVSSLFLLSVLLFVAVRLCRRSRAASVGRCSVPEGPFPGLVDVRGA  
ETLSQSYQYEVCLTGGPGTSEFKFLKPVISDIQAQGPGRKGEENSTFRNSFGFNIQ

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-26 ..

#### **Transmembrane domain:**

amino acids 687-711

#### **N-glycosylation sites.**

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

#### **Glycosaminoglycan attachment site.**

amino acids 28-32

#### **Tyrosine kinase phosphorylation sites.**

amino acids 394-402, 578-585

#### **N-myristoylation sites.**

amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,  
217-223, 324-330, 325-331, 471-477, 568-574, 759-765

#### **Amidation site.**

amino acids 781-785

#### **Aminoacyl-transfer RNA synthetases class-II signature 1.**

amino acids 117-138

#### **Cadherins extracellular repeated domain signature.**

amino acids 121-132, 230-241, 335-346, 439-450, 549-560





## **FIGURE 26**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92234

><subunit 1 of 1, 507 aa, 1 stop

><MW: 56692, pI: 5.22, NX(S/T): 3

MDPKLGRMAASLLAVLLLLLLERGMFSSPSPPPALLEKVYFYIDLHQDEFVQTLKEWVAIESD  
SVQPVPRFRQELFRMMAVAADTLQRLGARVASVDMGPQQLPDGQSLPIPPVILAE LGSDPTK  
GTVCFYGHLDVQPADRGDGLWLTDPYVLTEVDGKLYGRGATDNKGPVLAWINAVSAFRALEQD  
LPVNIKFIIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKPAITYGTRGNSY  
FMVEVKCRDQDFHSGTFFGILHEPMADLVALLGSLVDSSGHILVPGIYDEVVPLTEEEINTY  
KAIHLDLEEYRNSSRVEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRVIGK  
FSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTLGLHPWIANIDDTQYLAAKRAI  
RTVFGTEPDMIRDGSTIPIAKMFQEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLF  
AAFFLEMAQLH

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-26

#### **Transmembrane domain:**

273-292

#### **N-glycosylation sites.**

amino acids 322-326, 382-386, 402-406

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 400-404

#### **N-myristoylation sites.**

amino acids 89-95, 119-125, 162-168, 197-203, 242-248, 263-269,  
351-357

#### **Cell attachment sequence.**

amino acids 140-143

#### **ArgE / dapE / ACY1 / CPG:**

amino acids 156-167

## FIGURE 27

CTCGGCTGGATTTAAGGTTGCCGCTAGCCGCCTGGGAATTTAAGGGACCCACACTACCTTCC  
CGAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTTGTCATGGGACCTGTGCGGTT  
GGGAATATTGCTTTTCTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAGGAGG  
AGGACGATGACACAGAACGCTTGCCAGCAAATGCGAAGTGTGTAAGCTGCTGAGCACAGAG  
CTACAGGCGGAACTGAGTCGCACCGGTCGATCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCT  
GGATACAGGCAAGAGGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAAGGCTGGAAGAGG  
CCTTAGAGAATTTATGTGAGCGGATCCTGGACTATAGTGTTACGCTGAGCGCAAGGGCTCA  
CTGAGATATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCTAGTGCAGAAGGG  
GGTGAAGGTGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCAGCGTGGAGGTCACAT  
ACCTCAAGAAGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATTGTGGGAGACTGGTAC  
TTCCACCATCAGGAGCAGCCCCTACAAAATTTCTCTGTGAAGGTCATGTGCTCCCAGCTGC  
TGAAACTGCATGTCTACAGGAACTTGGACTGGAAAGGAGATCACAGATGGGGAAGAGAAAA  
CAGAAGGGGAGGAAGAGCAGGAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGGGGGAGACAAG  
ATGACCAAGACAGGAAGCCACCCCAAACCTTGACCGAGAAGATCTTTGACCCTTGCCTTTGAG  
CCCCCAGGAGGGGAAGGGATCATGGAGAGCCCTCTAAAGCCTGCACTCTCCCTGCTCCACAG  
CTTTCAGGGTGTGTTTATGAGTGACTCCACCCAAGCTTGTAGCTGTTCTCTCCCATCTAACC  
TCAGGCAAGATCCTGGTGAAACAGCATGACATGGCTTCTGGGGTGGAGGGTGGGGGTGGAGG  
TCCTGCTCCTAGAGATGAACTCTATCCAGCCCCCTTAATTGGCAGGTGTATGTGCTGACAGTA  
CTGAAAGCTTTCCTCTTTAACTGATCCCACCCCCACCCAAAAGTCAGCAGTGGCACTGGAGC  
TGTGGGCTTTGGGGAAGTCACTTAGCTCCTTAAGGTCTGTTTTTAGACCCTTCCAAGGAAGA  
GGCCAGAACGGACATTCTCTGCGATCTATATACATTGCCTGTATCCAGGAGGCTACACACCA  
GCAAACCGTGAAGGAGAATGGGACACTGGGTCATGGCCTGGAGTTGCTGATAATTTAGGTGG  
GATAGATACTTGGTCTACTTAAGCTCAATGTAACCCAGAGCCCACCATATAGTTTTATAGGT  
GCTCAACTTTCTATATCGCTATTAACTTTTTTCTTTTTTTCTA

## **FIGURE 28**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256

><subunit 1 of 1, 248 aa, 1 stop

><MW: 28310, pI: 4.63, NX(S/T): 0

MGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAELSRTGRSREVL  
ELGQVLDTGKRKRHVPYSVSETRLEEALENLCERILDYSVHAERKGSRLRYAKGQSQTMATLK  
GLVQKGVKVDLGIPLELWDEPSVEVTYLKKQCETMLEEFEDIVGDWYFHHQEQPLQNFLCEG  
HVLPAETAACLQETWTGKEITDGEEKTEGEEEQEEEEEEEEEEEEGGDKMTKTGSHPKLDREDL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-21

#### **cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 106-110

#### **N-myristoylation site.**

amino acids 115-121

#### **Amidation site.**

amino acids 70-74

## **FIGURE 29**

AAGTACTTGTGTCCGGGTGGTGGACTGGATTAGCTGCGGAGCCCTGGAAGCTGCCTGTCCTT  
CTCCCTGTGCTTAACCAGAGGTGCCC**ATG**GGTTGGACAATGAGGCTGGTCACAGCAGCACTG  
TTACTGGGTCTCATGATGGTGGTCACTGGAGACGAGGATGAGAACAGCCCGTGTGCCCATGA  
GGCCCTCTTGGACGAGGACACCCTCTTTTGCCAGGGCCTTGAAGTTTTCTACCCAGAGTTGG  
GGAACATTGGCTGCAAGGTTGTTCCCTGATTGTAACAACACTACAGACAGAAGATCACCTCCTGG  
ATGGAGCCGATAGTCAAGTTCCCGGGGGCCGTGGACGGCGCAACCTATATCCTGGTGATGGT  
GGATCCAGATGCCCCTAGCAGAGCAGAACCCAGACAGAGATTCTGGAGACATTGGCTGGTAA  
CAGATATCAAGGGCGCCGACCTGAAGAAAGGGAAGATTCAGGGCCAGGAGTTATCAGCCTAC  
CAGGCTCCCTCCCCACCGGCACACAGTGGCTTCCATCGCTACCAGTTCTTTGTCTATCTTCA  
GGAAGGAAAAGTCATCTCTCTCCTTCCCAAGGAAAACAAAACCTCGAGGCTCTTGGAAAATGG  
ACAGATTTCTGAACCGCTTCCACCTGGGCGAACCTGAAGCAAGCACCCAGTTCATGACCCAG  
AACTACCAGGACTCACCAACCCTCCAGGCTCCCAGAGGAAGGGCCAGCGAGCCCAAGCACAA  
AACCAGGCAGAGA**TAG**CTGCCTGCTAGATAGCCGGCTTTGCCATCCGGGCATGTGGCCACAC  
TGCTCACCACCGACGATGTGGGTATGGAACCCCCTCTGGATACAGAACCCCTTCTTTTCCAA  
ATTAAAAAAAAAATCATCAA

## **FIGURE 30**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92274

><subunit 1 of 1, 223 aa, 1 stop

><MW: 25402, pI: 8.14, NX(S/T): 1

MGWTMRLVTAALLGLMMVVTGDEDENSPCAHEALLDEDTLFCQGLEVFYPELGNIGCKVVP  
DCNNYRQKITSWMEPIVKFPGAVDGATYILVMVDPDAPSRAEPRQRFWRHWLVTDIKGADLK  
KGKIQGQELSAYQAPSPPAHSGFHRYQFFVYLQEGKVISLLPKENKTRGSKMDRFLNRFHL  
GEPEASTQFMTQNYQDSPTLQAPRGRASEPKHKTRQR

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-22

#### **N-glycosylation site.**

amino acids 169-173

#### **Tyrosine kinase phosphorylation site.**

amino acids 59-68

#### **N-myristoylation sites.**

amino acids 54-60, 83-89, 130-136

#### **Phosphatidylethanolamine signature.**

amino acids 113-157

## **FIGURE 31**

GTCGACCCACGCGTCCGAAGCTGCTGGAGCCACGATTCAGTCCCCTGGACTGTAGATAAAGA  
CCCTTTCTTGCCAGGTGCTGAGACAACCACACT**ATG**GAGAGGCACTCCAGGAGACGCTGATGG  
TGGAGGAAGGGCCGTCTATCAATCAATCACTGTTGCTGTTATCACATGCAAGTATCCAGAGG  
CTCTTGAGCAAGGCAGAGGGGATCCCATTTATTTGGGAATCCAGAATCCAGAAATGTGTTTG  
TATTGTGAGAAGGTTGGAGAACAGCCACATTGCAGCTAAAAGAGCAGAAGATCATGGATCT  
GTATGGCCAACCCGAGCCCGTGAAACCCTTCCTTTTCTACCGTGCCAAGACTGGTAGGACCT  
CCACCCTTGAGTCTGTGGCCTTCCCGGACTGGTTCATTGCCTCCTCCAAGAGAGACCAGCCC  
ATCATTCTGACTTCAGAACTTGGGAAGTCATACAACACTGCCTTTGAATTAAATATAAATGA  
**CTGA**ACTCAGCCTAGAGGTGGCAGCTTGGTCTTTGTCTTAAAGTTTCTGGTTCCCAATGTGT  
TTTCGTCTACATTTTCTTAGTGTCATTTTCACGCTGGTGCTGAGACAGGAGCAAGGCTGCTG  
TTATCATCTCATTTTATAATGAAGAAGAAGCAATTACTTCATAGCAACTGAAGAACAGGATG  
TGGCCTCAGAAGCAGGAGAGCTGGGTGGTATAAGGCTGTCTCTCAAGCTGGTGCTGTGTAG  
GCCACAAGGCATCTGCATGAGTGACTTTAAGACTCAAAGACCAAACACTGAGCTTTCTTCTA  
GGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGCATGACTAGCACA  
GAGCTGATCTCTGTTTCTGTTTTGCTTTATTCCCTCTTGGGATGATATCATCCAGTCTTTAT  
ATGTTGCCAATATAACCTCATTGTGTGTAATAGAACCTTCTTAGCATTAAGACCTTGTAACA  
AAAATAATTCTTGGGGTGGGTATGAAGATGCTTCAGAGCTCATGCGCGTTACCCACGATGGC  
ATGACTAGCACAGAGCTGATCTCTGTTTCTGTTTTGCTTTATTCCCTCTTGGGATGATATCA  
TCCAGTCTTTATATGTTGCCAATATAACCTCATTGTGTGTAATAGAACCTTCTTAGCATTAAG  
ACCTTGTAACAATAATAATTCTTGTGTTAAGTTAAATCATTTTTGTCCTAATTGTAATGTG  
TAATCTTAAAGTTAAATAAACTTTGTGTATTTATATAATAATAAAGCTAAAACTGATATAAA  
ATAAAGAAAGAGTAAACTG



[illegible]

amino acids 36-39



## **FIGURE 33**

GCGAGGCTGCACCAGCGCCTGGCACC**ATG**AGGACGCCTGGGCCTCTGCCCCGTGCTGCTGCTG  
CTCCTGGCGGGAGCCCCCGCCGCGCGGCCCACTCCCCGACCTGCTACTCCCGCATGCGGGC  
CCTGAGCCAGGAGATCACCCGCGACTTCAACCTCCTGCAGGTCTCGGAGCCCTCGGAGCCAT  
GTGTGAGATACCTGCCCAGGCTGTACCTGGACATACACAATTACTGTGTGCTGGACAAGCTG  
CGGGACTTTGTGGCCTCGCCCCCGTGTTGGAAAGTGGCCCAGGTAGATTCCCTTGAAGGACAA  
AGCACGGAAGCTGTACACCATCATGAACTCGTTCTGCAGGAGAGATTTGGTATTCCTGTTGG  
ATGACTGCAATGCCTTGGAATACCCAATCCCAGTGACTACGGTCCTGCCAGATCGTCAGCGC  
**TAA**GGGAACTGAGACCAGAGAAAGAACCCAAGAGAACTAAAGTTATGTCAGCTACCCAGACT  
TAATGGGCCAGAGCCATGACCCTCACAGGTCTTGTGTTAGTTGTATCTGAAACTGTTATGTA  
TCTCTCTACCTTCTGGAAAACAGGGCTGGTATTCCCTACCCAGGAACCTCCTTTGAGCATAGA  
GTTAGCAACCATGCTTCTCATTCCTTGACTCATGTCTTGCCAGGATGGTTAGATACACAGC  
ATGTTGATTTGGTCACTAAAAAGAAGAAAAGGACTAACAAGCTTCACTTTTATGAACAATA  
TTTTGAGAACATGCACAATAGTATGTTTTTTATTACTGGTTTAATGGAGTAATGGTACTTTTA  
TTCTTTCTTGATAGAAACCTGCTTACATTTAACCAAGCTTCTATTATGCCTTTTTCTAACAC  
AGACTTTCTTCACTGTCTTTCATTTAAAAAGAAATTAATGCTCTTAAGATATATATTTTACG  
TAGTGCTGACAGGACCCACTCTTTCATTGAAAGGTGATGAAAATCAAATAAAGAATCTCTTC  
ACATGGA

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
2	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
3	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
4	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
5	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81																			

```
><subunit 1 of 1, 136 aa, 1 stop
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MRTPGPLPVLLLLLAGAPAAARPTPPTCYSRMRALSQEITRDFNLLQVSEPSEPCVRYLPRLY  
LDIHNYCVLDKLRDFVASPPCWKVAQVDSLKDKARKLYTIMNSFCRRDLVFLLDDCNALEYF  
IPVTTVLPRQR

Signal peptide:

Tyrosine kinase phosphorylation site.

amino acids 60-69

N-myristoylation site.

amino acids 16-22

## FIGURE 35

GTCTCCGCGTCACAGGAACTTCAGCACCCACAGGGCGGACAGCGCTCCCCTCTACCTGGAGA  
CTTGACTCCCGCGCGCCCCAACCCCTGCTTATCCCTTGACCGTCGAGTGTCAGAGATCCTGCA  
GCCGCCAGTCCCGGCCCCCTCTCCCGCCCCACACCCACCCCTCCTGGCTCTTCCTGTTTTTAC  
TCCTCCTTTTTCATTCATAACAAAAGCTACAGCTCCAGGAGCCCAGCGCCGGGCTGTGACCCA  
AGCCGAGCGTGGAAGAATGGGGTTCCTCGGGACCGGCACTTGGATTCTGGTGTTAGTGCTCC  
CGATTCAAGCTTTCCCCAACCTGGAGGAAGCCAAGACAAATCTCTACATAATAGAGAATTA  
AGTGCAGAAAGACCTTTGAATGAACAGATTGCTGAAGCAGAAGAAGACAAGATTAAAAAAC  
ATATCCTCCAGAAAACAAGCCAGGTCAGAGCAACTATTCTTTTGTTGATAACTTGAACCTGC  
TAAAGGCAATAACAGAAAAGGAAAAAATTGAGAAAGAAAGACAATCTATAAGAAGCTCCCCA  
CTTGATAATAAGTTGAATGTGGAAGATGTTGATTCAACCAAGAATCGAAAACCTGATCGATGA  
TTATGACTCTACTAAGAGTGGATTGGATCATAAATTTCAAGATGATCCAGATGGTCTTCATC  
AACTAGACGGGACTCCTTTAACCGCTGAAGACATTGTCCATAAAATCGCTGCCAGGATTTAT  
GAAGAAAATGACAGAGCCGTGTTTGACAAGATTGTTTCTAACTACTTAATCTCGGCCTTAT  
CACAGAAAGCCAAGCACATACACTGGAAGATGAAGTAGCAGAGGTTTTACAAAAATTAATCT  
CAAAGGAAGCCAACAATTATGAGGAGGATCCCAATAAGCCCACAAGCTGGACTGAGAATCAG  
GCTGGAAAAATACCAGAGAAAGTGACTCCAATGGCAGCAATTCAAGATGGTCTTGCTAAGGG  
AGAAAACGATGAAACAGTATCTAACACATTAACCTTGACAAATGGCTTGGAAGGAGAACTA  
AAACCTACAGTGAAGACAACCTTTGAGGAACTCCAATATTTCCCAAATTTCTATGCGCTACTG  
AAAAGTATTGATTCAGAAAAAGAAGCAAAAGAGAAAGAAACACTGATTACTATCATGAAAAC  
ACTGATTGACTTTGTGAAGATGATGGTGAAATATGGAACAATATCTCCAGAAGAAGGTGTTT  
CCTACCTTGAAAACCTTGATGAAATGATTGCTCTTCAGACCAAAAACAAGCTAGAAAAAAAT  
GCTACTGACAATATAAGCAAGCTTTTCCCAGCACCATCAGAGAAGAGTCATGAAGAAACAGA  
CAGTACCAAGGAAGAAGCAGCTAAGATGGAAAAGGAATATGGAAGCTTGAAGGATTCCACAA  
AAGATGATAACTCCAACCCAGGAGGAAAGACAGATGAACCCAAAGGAAAAACAGAAGCCTAT  
TTGGAAGCCATCAGAAAAAATATTGAATGGTTGAAGAAACATGACAAAAGGGAAATAAAGA  
AGATTATGACCTTTCAAAGATGAGAGACTTCATCAATAAACAAGCTGATGCTTATGTGGAGA  
AAGGCATCCTTGACAAGGAAGAAGCCGAGGCCATCAAGCGCATTTATAGCAGCCTGTAAAAA  
TGGCAAAAGATCCAGGAGTCTTTCAACTGTTTCAGAAAACATAATATAGCTTAAAACACTTC  
TAATTCTGTGATTAAAATTTTTTGACCCAAGGGTTATTAGAAAGTGCTGAATTTACAGTAGT  
TAACCTTTTACAAGTGGTTAAAACATAGCTTTCTTCCCGTAAAAACTATCTGAAAGTAAAGT  
TGTATGTAAGCTGAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 36**

MGFLGTGTWILVLVLP IQAFPKPGGSQDKSLHNRELSAERPLNEQIAEAEEDKIKKTYPPEN  
KPGQSNYSFVDNLNLLKAITEKEKIEKERQSIRSSPLDNKLNVEDVDSTKNRKLIDDYDSTK  
SGLDHKFQDDPDGLHQLDGTPLTAEDIVHKIAARIYEENDRAVFDKIVSKLLNLGLITESQA  
HTLEDEVAEVLQKLISKEANNYEEDPNKPTSWTENQAGKIPKVTMAAIQDGLAKGENDET  
VSNTLTLTNGLERRTKTYSEDNFEELQYFPN FYALLKSIDSEKEAKEKETLITIMKTLIDFV  
KMMVKYGTISPEEGVSYLENLDEMIALQTKNKLEKNATDNISKLF PAPSEKSHEETDSTKEE  
AAKMEKEYGSLKDSTKDDNSNPGGKTDEPKGKTEAYLEAIRKNIEWLKKHDKKGNKEDYDLS  
KMRDFINKQADAYVEKGILDKEEA EAIKRIYSSL

### **N-glycosylation sites:**

amino acids 68-71, 346-349, 350-353

### **Casein kinase II phosphorylation site:**

amino acids 70-73, 82-85, 97-100, 125-128, 147-150, 188-191, 217-  
220, 265-268, 289-292, 305-308, 320-323, 326-329, 362-365, 368-  
341, 369-372, 382-385, 386-389, 387-390

### **N-myristoylation sites:**

amino acids 143-148, 239-244

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## **FIGURE 38**

MALPPGPAALRHTLLLLPALLSSGWGELEPQIDGQTWAERALRENERHAFTCRVAGGPGTPR  
LAWYLDGQLQEASTSRLLSVGGEAFSGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVIL  
NVQFKPEIAQVGAKYQEAQGPGLLVVLFALVRANPPANVTWIDQDGPVTVNTSDFLVLDAQN  
YPWLTNHTVQLQLRSLAHNLSVVATNDVGVTASLPAPGPSRHPSLISSDSNNLKLNNVRLP  
RENMSLPSNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLLTSQGFIRLPVLGYIY  
RVSSVSSDEIWL

### **N-glycosylation sites:**

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209,  
251-255, 280-284

### **Glycosaminoglycan attachment site:**

amino acids 23-27

### **Casein kinase II phosphorylation sites:**

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

### **N-myristoylation sites:**

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

## **FIGURE 39**

CGGGGACGGAAGCGGCCCCCTGGGCCCCGAGGGGCTGGAGCCGGGCGGGGGCG**ATG**TGGAGCGC  
GGGCCGCGGCGGGGCTGCCTGGCCGGTGCTGTTGGGGCTGCTGCTGGCGCTGTTAGTGCCGG  
GCGGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGCTGAAGCTGCTC  
AATACGCACCACCGCGTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCA  
GCAATCGGTGACCGGGCGTAGAGGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGCGGGCG  
GCTCGGAGGGCGGGTGCCCCGCGCGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACG  
CATGTGCTTACGGGCAAGAACCTGCACACGCACCACTTCCCGTCGCCGCTGTCCAACAACCA  
GGAGGTGAGTGCCTTTGGGGAAGACGGCGAGGGCGACGACCTGGACCTATGGACAGTGCGCT  
GCTCTGGACAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTG  
TTCCTGTCAGTCACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGG  
CATGCCCAGTGCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTA  
GTGTGGAGCCCTCTGCAGGTCACGATGAACTC**TGA**GTGTGTGGATGGATGGGTGGATGGAGG  
GTGGCAGGTGGGGCGTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTTGTAGGGGTCCTC  
AAGTGCCTTTGTGATTAAAGAATGTTGGTCTATGAAA

CGGGGACGGAAGCGGCCCCCTGGGCCCCGAGGGGCTGGAGCCGGGCGGGGGCG**ATG**TGGAGCGC  
GGGCCGCGGCGGGGCTGCCTGGCCGGTGCTGTTGGGGCTGCTGCTGGCGCTGTTAGTGCCGG  
GCGGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGCTGAAGCTGCTC  
AATACGCACCACCGCGTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCA  
GCAATCGGTGACCGGGCGTAGAGGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGCGGGCG  
GCTCGGAGGGCGGGTGCCCCGCGCGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACG  
CATGTGCTTACGGGCAAGAACCTGCACACGCACCACTTCCCGTCGCCGCTGTCCAACAACCA  
GGAGGTGAGTGCCTTTGGGGAAGACGGCGAGGGCGACGACCTGGACCTATGGACAGTGCGCT  
GCTCTGGACAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTG  
TTCCTGTCAGTCACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGG  
CATGCCCAGTGCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTA  
GTGTGGAGCCCTCTGCAGGTCACGATGAACTC**TGA**GTGTGTGGATGGATGGGTGGATGGAGG  
GTGGCAGGTGGGGCGTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTTGTAGGGGTCCTC  
AAGTGCCTTTGTGATTAAAGAATGTTGGTCTATGAAA



## **FIGURE 40**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857

><subunit 1 of 1, 221 aa, 1 stop

><MW: 23598, pI: 6.96, NX(S/T): 0

MWSAGRGGAAWPVLLGLLLALLVPGGGAAGTGAELVTCGSVLKLLNTHHRVRLHSHDIKYGS  
GSGQQSVTGVEASDDANSYWRIRGGSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPL  
SNNQEVSAFGEDGEGDDLDLWTVRCSGQHWEREAAVRFQHVGTSVFLSVTGEQYGSPIRGQH  
EVHGMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-28

#### **Glycosaminoglycan attachment site.**

amino acids 62-66

#### **N-myristoylation sites.**

amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93,  
91-97, 190-196

#### **Endoplasmic reticulum targeting sequence.**

amino acids 218-223

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## **FIGURE 41**

GTTGCTATGTTGCCCAGGCTGGTCTTGAAGTGCCTTGACCTCCTAAAGTGTTGGAACACAG  
ACGTGAGCCACTCCACCCAGCCTAAACTTCATCTTCTTTGGATGAGATGAACACTTTTAAC  
AAGAGAACAGGACTCTATATAAATCGCTGTGGGCTCACCACCTCTAAGGAGGAGCACTGACT  
GAAGACAGAAAAATTGATGAACTGAAGAAGACATGGTCCATTATGCCTTACAACTTACACA  
GTGCTTTGGGAATTCCAAAGTACTCAGTGGAGAGAGGTGTTTCAGGAGCCGTAGAGCCAGAT  
CGTCATC**ATG**TCTGCATTGTGGCTGCTGCTGGGCCTCCTTGCCCTGATGGACTTGTCTGAAA  
GCAGCAACTGGGGATGCTATGGAAACATCCAAAGCCTGGACACCCCTGGAGCATCTTGTGGG  
ATTGGAAGACGTCACGGCCTGAACTACTGTGGAGTTCGTGCTTCTGAAAGGCTGGCTGAAAT  
AGACATGCCATACCTCCTGAAATATCAACCCATGATGCAAACCATTTGGCCAAAAGTACTGCA  
TGGATCCTGCCGTGATCGCTGGTGTCTTGTCCAGGAAGTCTCCCGGTGACAAAATTCTGGTC  
AACATGGGCGATAGGACTAGCATGGTGCAGGACCCTGGCTCTCAAGCTCCCACATCCTGGAT  
TAGTGAGTCTCAGGTTTCCCAGACAACTGAAGTTCTGACTACTAGAATCAAAGAAATCCAGA  
GGAGGTTTCCAACCTGGACCCCTGACCAGTACCTGAGAGGTGGACTCTGTGCCTACAGTGGG  
GGTGCTGGCTATGTCCGAAGCAGCCAGGACCTGAGCTGTGACTTCTGCAATGATGTCCTTGC  
ACGAGCCAAGTACCTCAAGAGACATGGCTTC**TAA**CATCTCAGATGAAACCCAAGACCATGAT  
CACATATGCAGCCTCAAATGTTACACAGATAAACTAGCCAAGGGCACCTGTAACCTGGGAAT  
CTGAGTTTGACCTAAAAGTCATTAAAATAACATGAATCCCATTAATAAAAAAAAAAAAAA

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## **FIGURE 42**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96867

><subunit 1 of 1, 194 aa, 1 stop

><MW: 21431, pI: 8.57, NX(S/T): 0

MSALWLLLGLLALMDLSESSNWGCYGNIQSLDTPGASCGIGRRHGLNYCGVRASERLAEIDM  
PYLLKYQPMQTIGQKYCMDPAVIAGVLSRKSPGDKILVNMGDRTSMVQDPGSQAPTSWISE  
SQVSQTTEVLTTRIKEIQRRFPTWTPDQYLRGGLCAYSGGAGYVRSSQDLSCDFCNDVLARA  
KYLKRHGF

**Important features of the protein:**

**Signal peptide:**

amino acids 1-19

**N-myristoylation sites.**

amino acids 23-29, 26-32, 35-41, 45-51, 50-56, 76-82, 156-162

**Amidation site.**

amino acids 40-44

## **FIGURE 43**

TTGAAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTCTCAGGACCCTCGCC**ATG**AAAG  
CCCTTATGCTGCTCACCCTGTCTGTTCTGCTCTGCTGGGTCTCAGCTGACATTCGCTGTCAC  
TCCTGCTACAAGGTCCCTGTGCTGGGCTGTGTGGACCGGCAGTCCTGCCGCCTGGAGCCAGG  
ACAGCAATGCCTGACAACACATGCATACCTTGGTAAGATGTGGGTTTTCTCCAATCTGCGCT  
GTGGCACACCAGAAGAGCCCTGTCAGGAGGCCTTCAACCAAACCAACCGCAAGCTGGGTCTG  
ACATATAACACCACCTGCTGCAACAAGGACAACCTGCAACAGCGCAGGACCCCGGCCCACTCC  
AGCCCTGGGCCTTGTCTTCCTTACCTCCTTGGCTGGCCTTGGCCTCTGGCTGCTGCAC**TGAG**  
ACTCATTCCATTGGCTGCCCCCTCCTCCACCTGCCTTGGCCTGAGCCTCTCTCCCTGTGTCT  
CTGTATCCCCTGGCTTTACAGAATCGTCTCTCCCTAGCTCCCATTTCTTTAATTAAACACTG  
TTCCGAGTGGTCTCCTCATCCATCCTTCCACCTCACACCCTTCACTCTCCTTTTTCTGGGT  
CCCTTCCCACCTTCCTTCCAGGACCTCCATTGGCTCCTAGAAGGGCTCCCCACTTTGCTTCCT  
ATACTCTGCTGTCCCCTACTTGAGGAGGGATTGGGATCTGGGCCTGAAATGGGGCTTCTGTG  
TTGTCCCCAGTGAAGGCTCCCACAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCA  
AACCAGGCTCCCATATGTACCCCATCCCCCATACTCACCTCTTTCCATTTTGAGTAATAAA  
TGTCTGAGTCTGGAAAAAAAAAAAAAAAAAAAAA

## **FIGURE 44**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96878

><subunit 1 of 1, 125 aa, 1 stop

><MW: 13821, pI: 8.60, NX(S/T): 2

MKALMLLTLSVLLCWVSADIRCHSCYKVPVLGCVDRQSCRLEPGQQCLTTHAYLGKMWVFSN  
LRCGTPEEPCQEAFNQTNRKLGTYNTTCENKDNCNSAGPRPTPALGLVFLTSLAGLGLWLLH

### **Important features of the protein:**

#### **Signal peptide:**

amino acids 1-18

#### **N-glycosylation sites.**

amino acids 77-81, 88-92

#### **N-myristoylation site.**

amino acids 84-90

#### **Ly-6 / u-PAR domain protein signature.**

amino acids 85-98

## **FIGURE 45**

ACGGGCCGCAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGCGGGCTGCAGCTCTGCA  
GTCGGGCCGTTTCCTTCGCCGCCGCCAGGGGTAGCGGTGTAGCTGCGCAGCGTCGCGCGCGCT  
ACCGCACCCAGGTTTCGGCCCCGTAGGCGTCTGGCAGCCCCGGCGCCATCTTCATCGAGCGCC**AT**  
**GGCCGCAGCCTGCGGGCCGGGAGCGGCCGGGTACTGCTTGCTCCTCGGCTTGCA**TTTGTTTC  
TGCTGACCGCGGGCCCTGCCCTGGGCTGGAACGACCCTGACAGAATGTTGCTGCGGGATGTA  
AAAGCTCTTACCCTCCACTATGACCGCTATAACCACCTCCCGCAGGCTGGATCCCATCCCACA  
GTTGAAATGTGTTGGAGGCACAGCTGGTTGTGATTCTTATACCCCAAAGTCATACAGTGTC  
AGAACAAGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCA  
TACAAATTTGGAAAACTGTGGTGAGCTGTGAAGGCTATGAGTCCTCTGAAGACCAGTATGT  
ACTAAGAGGTTCTTGTGGCTTGGAGTATAATTTAGATTATACAGAACTTGGCCTGCAGAAAC  
TGAAGGAGTCTGGAAAGCAGCACGGCTTTGCCTCTTTCTCTGATTATTATTATAAGTGGTCC  
TCGGCGGATTCCTGTAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTT  
TGTAGTCTATAAGCTGTTCTGAGTGACGGGCAGTATTCTCCTCCACCGTACTCTGAGTATC  
CTCCATTTTCCCACCGTTACCAGAGATTCACCAACTCAGCAGGACCTCCTCCCCCAGGCTTT  
AAGTCTGAGTTCACAGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTTTGGCAGTGC  
TTTTACAGGACAACAAGGATATGAAAATTCAGGACCAGGGTTCTGGACAGGCTTGGGAACTG  
GTGGAATACTAGGATATTTGTTTGGCAGCAATAGAGCGGCAACACCCTTCTCAGACTCGTGG  
TACTACCCGTCCTATCCTCCCTCCTACCCTGGCACGTGGAATAGGGCTTACTACCCCTTCA  
TGGAGGCTCGGGCAGCTATTCGGTATGTTCAAACCTCAGACACGAAAACCAGAACTGCATCAG  
GATATGGTGGTACCAGGAGACGAT**TAA**AGTAGAAAGTTGGAGTCAAACACTGGATGCAGAAAT  
TTTGGATTTTTCATCACTTTCTCTTTACAAAAAAGTACTACCTGTTAACAATTGGGAAAAG  
GGGATATTCAAAAGTTCTGTGGTGTTATGTCCAGTGTAGCTTTTTTGTATTCTATTATTGAG  
GCTAAAAGTTGATGTGTGACAAAATACTTATGTGTTGTATGTCAGTGTAACATGCAGATGTA  
TATTGCAGTTTTTGAAGTGATCATTACTGTGGAATGCTAAAAATACATTAATTTCTAAAC  
CTGTGATGCCCTAAGAAGCATTAAGAATGAAGGTGTTGTACTAATAGAACTAAGTACAGAA  
AATTTAGTTTTAGGTGGTTGTAGCTGATGAGTTATTACCTCATAGAGACTATAATATTCTA  
TTTGGTATTATATTATTGATGTTTGCTGTTCTTCAAACATTTAAATCAAGCTTTGGACTAA  
TTATGCTAATTTGTGAGTTCTGATCACTTTTGAGCTCTGAAGCTTTGAATCATTGAGTGGTG  
GAGATGGCCTTCTGGTAACTGAATATTACCTTCTGTAGGAAAAGGTGGAAAATAAGCATCTA  
GAAGGTGTTGTGAATGACTCTGTGCTGGCAAAAATGCTTGAAACCTCTATATTTCTTTTCGT  
TCATAAGAGGTAAAGGTCAAATTTTTCAACAAAAGTCTTTTAATAACAAAAGCATGCAGTTC  
TCTGTGAAATCTCAAATATTGTTGTAATAGTCTGTTTCAATCTTAAAAAGAATCA

## **FIGURE 46**

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889

><subunit 1 of 1, 339 aa, 1 stop

><MW: 36975, pI: 7.85, NX(S/T): 1

MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDPIP  
QLKCVGGTAGCDSYTPKVIQCQNKGWGDGYDVQWECKTDLDIAYKFGKTVVSCEGYESSEDQY  
VLRGSCGLEYNLDYTELGQLKESGKQHGFASFSDYYYKWSSADSCNMSGELITIVVLLGIA  
FVVYKLFLLSDGQYSPPPYSEYPPFSHRYQRFTNSAGPPPPGFKSEFTGPQNTGHGATSGFGS  
AFTGQQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDSWYYPSYPPSYPGTWNRAYSPL  
HGGSGSYSVCSNSDTKTRTASGYGGTRRR

### **Signal peptide:**

amino acids 1-30

### **Transmembrane domain:**

amino acids 171-190

### **N-glycosylation site.**

amino acids 172-176

### **Glycosaminoglycan attachment sites.**

amino acids 244-248, 259-263, 331-335

### **Tyrosine kinase phosphorylation site.**

amino acids 98-106

### **N-myristoylation sites.**

amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,  
270-276, 278-284, 312-318